

Db 675 Q1RAIDHTGKVVSAVLPGGQANPMTEANGHQAVALAG-----GHHEM 720
QY 565 STAIGNAVYVFPALP 578
Db 721 MTPVSDQIVVYALP 734

RESULT 5
US-08-169-927-2
Sequence 2, Application US/08169927
Patent No. 5783441

GENERAL INFORMATION:

APPLICANT: Carl, Mitchell
APPLICANT: Dobson, Michael E.

APPLICANT: Ching, Wei Mei
APPLICANT: Dasch, Gregory A.

TITLE OF INVENTION: Gene and Protein Applicable to the
Preparation of Vaccines for Rickettsia prowazekii and
the Detection of Both

TITLE OF INVENTION: Rickettsia typhi and the Detection of Both

NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Counsel, Naval Medical R & D Command
STREET: Bldg. 1, T-12, 8901 Wisconsin Ave.
CITY: Bethesda

STATE: MD
COUNTRY: USA

ZIP: 20889-5606

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/169,927
FILING DATE:

CLASSIFICATION: 435
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/742,138
FILING DATE: 08/09/91

ATTORNEY/AGENT INFORMATION:
NAME: Spevack, A. David

REGISTRATION NUMBER: 24,743
REFERENCE/DOCKET NUMBER: 75,976

TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 295-6759

TELEFAX: (301) 295-1022
INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:
LENGTH: 1612 amino acids
TYPE: amino acid

TOPOLOGY: linear
MOLECULE TYPE: protein

US-08-169-927-2

Query Match 3.8%; Score 118.5; DB 1; Length 1612;
Best Local Similarity 18.3%; Pred. No. 0.09;

Matches 126; Conservative 85; Mismatches 231; Indels 247; Gaps 31;

QY 56 LPTITENVGOLDVWARGNQPKYVYVPLIHGCVWYLANPGVYIAID-----AKHG 108
Db 613 INELVFNENNSVVD-----NHFTYLTITKTN-----AANOGQIYAADPLNTTTLADG 661

QY 109 DLIWEHRRLPNT-----ATLNSFEPTRGALYGTNYFVSMDNHLVALDPTAGQVTF 162
Db 662 TNLGSAENPLSTHFAFDKAMDSILNVGKGVLYA-----NNTTNDANVGSILHF 712

QY 163 DVVRGGGEMDVNS-----SGPIYANGVYVASTQYSPFGCEVSGHDSATGELMR--NY 216
Db 713 ---RSGGTSIVSGTGGGQGHKLNILNDNGTVKFLGDTTF--NGGTXIEGSIILQISNN 768

QY 217 FIPRAEEDGETMGNDYENKRWMTGANGQITTPVT----- 251

Db 769 YTTDVHESADN-----TGTLEFVNTDPTVYTLNKGAYFGVLYKOVYISGPGNIV 817
QY 252 -----NLVHGSTAVGPASETORKP-----GGTLXGNTFRAY 285
Db 818 FNEIGNVGIHGIANSISFENASLSTLFLPSGTPLDVLFIKSTVGNGYVDNFNPIYV 877
QY 286 -----RPDGEIYWRQ-----TLPRDNMDQECTEAMVTNVDPSTMEGLASINPN 334
Db 878 VSGIDSMINNGOILIGDKKNIIALSIGSDN-----SIVANMTLYSGIRTTKNN 925
QY 335 AATGERRVLTGVPECKTSTMQFPAETGEFLMAR---DTNYONNIESIDENGIYTVVEDAI 391
Db 926 --GGTVILSGGMNNRPTIYGLGLENGSPKAKYVTTTDDVNNIGSIANN--VTINDVTF 981
QY 392 LKELDEYDVCPFLGGRDWP-----AALNPDGIVFIPLNVCYDMAVDOEFT---SM 444
Db 982 LTTGGI-----AGTDEDAKITLGSVGNANVAF-----VDSFSPSRSM 1020
QY 445 DVYNTSN---VTKLPPGKMDIGRIDAIIDISTGRTIHSVRAAANY----- 486
Db 1021 IVATQANKGTIVYL--GNALVSNIGSLDPPVASVRFPGNDSGAGLGQGNITYSONIDFGTYN 1078
QY 487 ---SPVLSTGGVLFNGGTDYFRFALSOETGETLM--QTRLATVAS-----GOAISY 533
Db 1079 LTLINSNVILGGGTTALNGEIDLTLNNLIFANGSTWGDNTSITTLNVSNGNIQOVYA 1138
QY 534 E-----VDGQYVAIAGGCVSYGSL---NSALAGERY---SM 563
Db 1139 EDAQVNAVTTGTTTIRIKIODNANANFSGTQAYVTLIOGARFNGTLAPNPAVAGSNIFVY 1198
QY 564 ---DS-----TAIGNA 571
Db 1199 ELIRDSNODVLTFRVDVYLVNVTAVGNS 1227

RESULT 6

US-07-642-734C-4
Sequence 4, Application US/07642734C
Patent No. 5824513

GENERAL INFORMATION:

APPLICANT: Katz, L
APPLICANT: Donadio, S

APPLICANT: McAlpine, J B
TITLE OF INVENTION: Recombinant DNA Method for Producing
Erythromycin Analogs

NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:

ADDRESSEE: Edward H. Gorman
STREET: Abbott Laboratories D377/AP6D-2 One Abbott
CITY: Park Rd

STATE: IL
COUNTRY: US

ZIP: 60064-3500

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/642,734C
FILING DATE: 17-JAN-91

CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:

NAME: Danckers, Andreas M
REGISTRATION NUMBER: 32652

REFERENCE/DOCKET NUMBER: 4952.US.01
TELECOMMUNICATION INFORMATION:

TELEPHONE: 708-937-9396
TELEFAX: 708-938-2623

INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:

LENGTH: 3567 amino acids

TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-642-734C-4

Query Match 3.7%; Score 115; DB 2; Length 3567;
Best Local Similarity 22.8%; Pred. No. 0.71; Indels 174; Gaps 27;
Matches 133; Conservative 50; Mismatches 226;

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21 AFAQVTEVTDELLANPPAGEM-----ISYQONQENRHSPLTQITTEVNGQLQIYW 71
2911 AFAVIAVTDRLRLARVDDG-WSDADAAPVIAV-----TTAHYALHDLGLAGAGSVLIH 2964
72 ARGMPGKVQVYPLIHGCVYLANPGDVIOAIDAKTGDLIWEHRQLPNATLNSGEPT 131
2965 AAAGVGMAAVALARRAGAEVLATAG-----PAKHG-----TLRALG----- 3001
132 RGMALYGTNVYFVSMNHLVALDTATGQVTEVDYR--GQGEDMVNS-----SGPIV 181
3002 -----LDEHIIASSRETCFARKFRERTGKRGVDVYVLSLIGELLDESADLL 3047
182 A-NGVIV-AGST-----CQSPGCFVSGHDSATGELMRNFIPRAGEGDETWG 230
3048 AEDGVFVEMKTDLRDAGDFRGKRYAPFDLGEAG--DRLGLILEVYVGLLAGELD----- 3101
231 NDYERAMWTGAM---GQITVDPVTNLVHYGSTAV--GPASETORGT---PGTLYGTNTR 282
3102 -----RLPVSAMELGSAAPALQHMRSRGRHYKLVLPAPVDDPGVYLITGGR--GTIGR 3154
283 FAVRPDTEIYWRQTL-PRDNMDQECTFEMMYTNVDVQSTMEGLQSLNPNAT----- 337
3155 LLARILVTEHGVRLHLIVSRGADAPGSDDELRAETEDLGASAEIACDTRADRLALSLLD 3214
338 GERRVLTVGPCKTGMQFPAETGEFLMARPTNYNNMIESIDENGIYT--VNEDAILKELD 396
3215 GLPRLTGVVHAAGVL-----ADGLVTSIDEPRAVQVYLR 3248
397 VEYDVCPFFLGGRDPPSALNPDSGIYFIPLNNVCYDMAVDOFTSMDYNTSNV----- 452
3249 AKVDAA-----WNLHELTANTGLSFEVLFSSAASVLA-----GPGQGYAAANESLNA 3296
453 -----TKLPKG-----DMGRIDAIDISTGRTLMSEVERAANYSP 488
3297 LLAALRTKGLPAKALGWMQASMTSGLDRIAR-----TGVAALPTERRALLFLDS 3349
489 VLTSGGVLFNGGTDTRYFRALSQETGETL--WQTRLATVASSQA 530
3350 ALRGGEVVFLPINSIRSLARRAEFPEVLKGMVRAKLRAAQA 3392

```

RESULT 7

US-08-439-009A-4
Sequence 4, Application US/08439009A
Patent No. 6004787

GENERAL INFORMATION:

APPLICANT: Donadio, S
APPLICANT: Kacz, L
APPLICANT: McAlpine, J B
TITLE OF INVENTION: Method of Directing Biosynthesis of
TITLE OF INVENTION: Specific Polypeptides
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSER: Steven F. Weinstein
STREET: Abbott Laboratories D377/APD-2 One Abbott
STREET: Park Rd
CITY: Abbott Park
STATE: IL
COUNTRY: US
ZIP: 60064-3500

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/439,009A
FILING DATE: 11-MAY-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Casuto, Dianne
REGISTRATION NUMBER: 40,943
REFERENCE/DOCKET NUMBER: 4952, US.D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847-938-3137
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 3567 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-439-009A-4

Query Match 3.7%; Score 115; DB 3; Length 3567;
Best Local Similarity 22.8%; Pred. No. 0.71;
Matches 133; Conservative 50; Mismatches 226; Indels 174; Gaps 27;

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21 AFAQVTEVTDELLANPPAGEM-----ISYQONQENRHSPLTQITTEVNGQLQIYW 71
2911 AFAVIAVTDRLRLARVDDG-WSDADAAPVIAV-----TTAHYALHDLGLAGAGSVLIH 2964
72 ARGMPGKVQVYPLIHGCVYLANPGDVIOAIDAKTGDLIWEHRQLPNATLNSGEPT 131
2965 AAAGVGMAAVALARRAGAEVLATAG-----PAKHG-----TLRALG----- 3001
132 RGMALYGTNVYFVSMNHLVALDTATGQVTEVDYR--GQGEDMVNS-----SGPIV 181
3002 -----LDEHIIASSRETCFARKFRERTGKRGVDVYVLSLIGELLDESADLL 3047
182 A-NGVIV-AGST-----CQSPGCFVSGHDSATGELMRNFIPRAGEGDETWG 230
3048 AEDGVFVEMKTDLRDAGDFRGKRYAPFDLGEAG--DRLGLILEVYVGLLAGELD----- 3101
231 NDYERAMWTGAM---GQITVDPVTNLVHYGSTAV--GPASETORGT---PGTLYGTNTR 282
3102 -----RLPVSAMELGSAAPALQHMRSRGRHYKLVLPAPVDDPGVYLITGGR--GTIGR 3154
283 FAVRPDTEIYWRQTL-PRDNMDQECTFEMMYTNVDVQSTMEGLQSLNPNAT----- 337
3155 LLARILVTEHGVRLHLIVSRGADAPGSDDELRAETEDLGASAEIACDTRADRLALSLLD 3214
338 GERRVLTVGPCKTGMQFPAETGEFLMARPTNYNNMIESIDENGIYT--VNEDAILKELD 396
3215 GLPRLTGVVHAAGVL-----ADGLVTSIDEPRAVQVYLR 3248
397 VEYDVCPFFLGGRDPPSALNPDSGIYFIPLNNVCYDMAVDOFTSMDYNTSNV----- 452
3249 AKVDAA-----WNLHELTANTGLSFEVLFSSAASVLA-----GPGQGYAAANESLNA 3296
453 -----TKLPKG-----DMGRIDAIDISTGRTLMSEVERAANYSP 488
3297 LLAALRTKGLPAKALGWMQASMTSGLDRIAR-----TGVAALPTERRALLFLDS 3349
489 VLTSGGVLFNGGTDTRYFRALSQETGETL--WQTRLATVASSQA 530
3350 ALRGGEVVFLPINSIRSLARRAEFPEVLKGMVRAKLRAAQA 3392

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RESULT 8

US-08-700-651-5
Sequence 5, Application US/08700651B
Patent No. 6015882

GENERAL INFORMATION:

APPLICANT: PETERSEN, CAROLYN
APPLICANT: LEECH, JAMES

; APPLICANT: NELSON, RICHARD, C.
 ; APPLICANT: GUT, JIRI
 ; TITLE OF INVENTION: VACCINES, ANTIBODIES, PROTEINS, GLYCOPROTEINS, DNAS AND RNAS
 ; TITLE OF INVENTION: FOR PROPHYLAXIS AND TREATMENT OF Cryptosporidium parvum
 ; TITLE OF INVENTION: INJECTIONS
 ; FILE REFERENCE: 480.19-4(HV)
 ; CURRENT APPLICATION NUMBER: US/08/700,651B
 ; CURRENT FILING DATE: 1997-08-14
 ; EARLIER APPLICATION NUMBER: 08/415,751
 ; EARLIER FILING DATE: 1995-04-03
 ; NUMBER OF SEQ ID NOS: 15
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 5
 ; LENGTH: 1721
 ; TYPE: PRT
 ; ORGANISM: Cryptosporidium parvum
 ; US-08-700-651-5

Query Match 3.7%; Score 114.5; DB 3; Length 1721;
 Best Local Similarity 20.2%; Pred. No. 0.24;
 Matches 140; Conservative 82; Mismatches 227; Indels 245; Gaps 38;

Oy 25 VTPVDELLAMPAGEMWISYQONE-----NTRHSPLOITTEVNGQLQLVWARGMOP 77
 Db 979 IDPTTG-LPEPPTGHLINPTNNMTDSSPAGAYKAYVNSGIKTDV-----YGLPV 1029
 Oy 78 GKVOVTPLIHGDVWVLANPGVIOAIDAKTGDIWEHRQLPNATINSCEPTRGMAHY 137
 Db 1030 GEIGLGP-----KDPGSDI-PFNTSTGEIV-----DSTGKPIN 1062
 Oy 138 GTNVEYSMDNHLVALDPTAGQVTEVDVROGEDMWSNSGPVYANGVYAGSTCQSPF 197
 Db 1063 NSTAGIVSGKRGKLPIDENGNL-ED-----PSTMLPIDGNNGQLNPNPT 1105
 Oy 198 GCFPSGDSAT-----GEELMRNFIP--RAGEGDEPTWANDYEARMGAMCOITYDPV 250
 Db 1106 NSTVSGSTGTTKPKKPIPVNGGAVPDEBAKQADK--GKD--GLIYPTNSINKDPV 1160
 Oy 251 TNLVHGSTA--VGPASETORGTPG-----GLTGTTRRAVRP 287
 Db 1161 TMTQYMTGNTIINP--ETCKVLPGLPSGLANPSPNTPOQDETETGKPYDVTGLPYDP 1218
 Oy 288 DTGEIYVRRHOTLPDND--WDQECTEEMVYN-----VDVQ--PSTEMEGLQS---- 330
 Db 1219 STGEIIDPATKLPKIPGSVAGDEILTEVLNITDEVGLPIDLETGLPRPVSGLPOLPNC 1278
 Oy 331 --INP-----NAATG-----ERRVLTGVPCKTGT--MMQPD-----AETG 361
 Db 1279 TLVDPSSKKRIPGSHSGFTIGTSGEOSHEDPSTGKPLDPNTGLHPFDEDSGLINPETG 1338
 Oy 362 EFLMARDTNY-----ONMIESIDENGIVTYNE-----PAI----- 391
 Db 1339 DKLGSHSGTFMPVPGKPGGENGIMTPQOILEAL--NMLPISNEVINISPRSSDAVPR 1396
 Oy 392 -----LKEIDVEYDVCPTFLG-----RDWPSAAL--NPDSGIYFIPLN 428
 Db 1397 PNTTMMNKISGQTYVDGKTKTILGSAASVIAHTALGPTDPTTGLPSPTGLPIFEGF 1456
 Oy 429 NTCYDMAVDO-----EFTSMDEVYNTSNVTKLPCKDKMIGRIDAIDISTGRLMSVERAA 483
 Db 1457 NVLVDPQTEQJIKGVPYSLVYKKNVYTEAAGL-----PVDPKTGPIDPI----- 1505
 Oy 484 ANYSPLYLSTG-----GGVLFNGTDTRYFRA-----LSOETGELMOT----- 520
 Db 1506 -SYLFPKANGCELIDPISCKYFGSGIAGFISCKAQSOSKSSDSSGNIPDPSTMPYDPCG 1564
 Oy 521 RLATYASGAISYEVDMQYVAIAG-----GCV 548
 Db 1565 KLIDPESGIAIDNSVSGV-FATVPSTAAPKKGV 1597

RESULT 9

US-08-219-262B-10
 ; Sequence 10; Application US/08219262B
 ; Patent No. 5788970
 ; GENERAL INFORMATION:

; APPLICANT: VAKHARIA, VIKRAM
 ; APPLICANT: SNYDER, DAVID B
 ; APPLICANT: MENDEL-WHERSAT, STEPHANIE A
 ; TITLE OF INVENTION: CHIMERIC INFECTIOUS BURSAL DISEASE VIRUS
 ; TITLE OF INVENTION: CDNA CLONES, EXPRESSION PRODUCTS AND VACCINES BASED
 ; TITLE OF INVENTION: THEREON
 ; NUMBER OF SEQUENCES: 15
 ; CORRESPONDENCE ADDRESS:

; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT
 ; STREET: 1755 S. JEFFERSON DAVID HIGHWAY, FOURTH FLOOR
 ; CITY: ARLINGTON
 ; STATE: VIRGINIA
 ; COUNTRY: USA
 ; ZIP: 22202

COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/219,262B
 ; FILING DATE: 29-MAR-1994

CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:
 ; NAME: OBLON, NORMAN F
 ; REGISTRATION NUMBER: 24,618
 ; REFERENCE/DOCKET NUMBER: 2747-047-27
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (703) 413-3000
 ; TELEFAX: (703) 413-2220

; TELEX: 248855 OPAT UR
 ; INFORMATION FOR SEQ ID NO: 10:
 ; SEQUENCE CHARACTERISTICS:

; LENGTH: 1012 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS:

; TOPOLOGY: unknown

; MOLECULE TYPE: protein

; ORIGINAL SOURCE:

; ORGANISM: Infectious bursal disease virus

; STRAIN: OH
 ; US-08-219-262B-10

Query Match 3.7%; Score 113.5; DB 1; Length 1012;
 Best Local Similarity 23.0%; Pred. No. 0.12;
 Matches 94; Conservative 49; Mismatches 139; Indels 127; Gaps 22;

Oy 250 VTNLVHGSTAV-----GPAS-----ETORGTPGTYLGTNTRF 283
 Db 1 MTNLMDHTQOILVPLRSLMLMPTGPASIPDTELEKHTLRSETSYNLTVDGSGLIYVF 60
 Oy 284 AVRPDTGIVVRRHOTLPDND--NNDQECTEEMVYN-----NVDVOPSTE 324
 Db 61 PGFP--GSVGAHAYTLLOSNGSYOPDQ-----MLTAAONLPSVYNYCRVLSRSLTVRSSTL 113
 Oy 325 MEGLOSTNP--NAATGRRVLTGVPCKTGTMMQPDATGTFELMARDTNYNOMIEST-- 378
 Db 114 PGVYALNGTINAVT-----FQGSLSL--TDTSYGLMSATANIN 152
 Oy 379 DENGIVTVNEDAILKEIDVEYDVCPTFLGGRDWPSSAALNPDSGIYFIPLNNVC----- 431
 Db 153 DKIGNVAVGEGVVLSPSTYDLSYVRLGD--PIPAAGLDP-----KLMAOTDSSDRR 204
 Oy 432 -YDMMAVDO--EF-----TSMDVYNTSNVTKLPCKDKMIGRIDAIDISTGRLTW- 477
 Db 205 VYTVTADEYQESSQLIPSGVKTTLFTANIDALTSVGGELIFSOVTHSIEVDVITYF 264
 Oy 478 -----SVERAANYSPLYLSTGGVLFN--GGTDTRYFALSQETGELMOTRLATVAS 527

Db 265 IGDGTEVTVKAVATDGLTTGTNNLVPFNLGPTSETPTPTSMKLEVTYKRGCT--A 322
QY 528 GOAISYEVDMQYVVALAGGVSYGSLN--SALAGERVSTAGNAYV 574
Db 323 GDPISWTVSGTLAVTVGG--NYPGALRPVTLVAYERV--AAGSVTV 366

RESULT 10

US-09-031-655-10
Sequence 10, Application US/09031655
Patent No. 6017759

GENERAL INFORMATION:
APPLICANT: VAKHARIA, VIKRAM
APPLICANT: SNYDER, DAVID B
APPLICANT: MENDEL-WHERSAT, STEPHANIE A
TITLE OF INVENTION: CHIMERIC INFECTIOUS BURSAL DISEASE VIRUS
TITLE OF INVENTION: CDNA CLONES, EXPRESSION PRODUCTS AND VACCINES BASED
TITLE OF INVENTION: THERON
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT
STREET: 1755 S. JEFFERSON DAVID HIGHWAY, FOURTH FLOOR
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: USA
ZIP: 22202

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/031,655

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/219,262
FILING DATE: 29-MAR-1994

ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F

REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 2747-047-27

TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000

TELEFAX: (703) 413-2220
TELEX: 248855 OPAT UR

INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:

LENGTH: 1012 amino acids
TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: unknown

MOLECULE TYPE: protein

ORIGINAL SOURCE:

ORGANISM: Infectious bursal disease virus
STRAIN: OH

US-09-031-655-10

Query Match 3.7%, Score 113.5; DB 3; Length 1012;
Best Local Similarity 23.0%; Pred. No. 0.12;
Matches 94; Conservative 49; Mismatches 139; Indels 127; Gaps 22;

QY 250 VNNIVHYSTAY-----GPAS-----EPQKTPGGTLYGNTNTRF 283
Db 1 VNNIVHYSTAY-----GPAS-----EPQKTPGGTLYGNTNTRF 60
QY 284 AVRPDTGEIVMRHQTLPD--NMDQECTFEEMAVT-----NVDVQPSST 324
Db 61 PGP--GSVVAHAYTLQSGSYQFDQ---MLTPAONLPVSYNYCRVLSRLVRSSTL 113
QY 325 MEGLOSINP--NAATGERAVLTGVECKTGTMTQDAEIGEFIMADTYNQNNEISI----- 378

Db 114 PGGYVALNNTINAV-----FGSLSEL---TDYSYNGLSMSTANIN 152
QY 379 DENGIVTVNEDAILKELDEVYDVCPTFLGGRWPSAALNPDSGITFPLNNVC----- 431
Db 153 DKIGNVLVEGVTVLSLPTSYDLSTYVRIGD--PIPAAGIDP-----KIMATCDSSDRP 204
QY 432 -YDMAAVDO-EF-----TSMDEVNTSNVTKLPKPKDMI-GRIDALDISTGRTLM- 477
Db 205 VYTVTAADDEYQFSSQLIPSGVKTTLFTANIDALHLSVGGELIFSQVTHISEVETIIF 264
QY 478 -----SVERAANYSPVLSTGGVLFN--GGTDYFRALSOETGETLMQRTIATVAS 527
Db 265 IGDGTEVTVKAVATDGLTTGTNNLVPFNLGPTSETPTPTSMKLEVTYKRGCT--A 322
QY 528 GOAISYEVDMQYVVALAGGVSYGSLN--SALAGERVSTAGNAYV 574
Db 323 GDPISWTVSGTLAVTVGG--NYPGALRPVTLVAYERV--AAGSVTV 366

RESULT 11

US-08-542-003-6
Sequence 6, Application US/08542003
Patent No. 5864013

GENERAL INFORMATION:
APPLICANT: Goldberg, Edward B.
TITLE OF INVENTION: MATERIALS FOR THE PRODUCTION OF
TITLE OF INVENTION: NANOMETER STRUCTURES AND USE THEREOF
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie and Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: US
ZIP: 10036

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/542,003

FILING DATE: 13-OCT-1995

CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:
NAME: Mistock, S. Leslie

REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 8471-0005-999

TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090

TELEFAX: 212-869-8864
TELEX: 66441 PENNIE

INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:

LENGTH: 1026 amino acids
TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

ORIGINAL SOURCE:

ORGANISM: Bacteriophage T4

IMMEDIATE SOURCE:

CLONE: p37 amino acid

US-08-542-003-6

Query Match 3.6%, Score 112.5; DB 2; Length 1026;
Best Local Similarity 20.3%; Pred. No. 0.16;
Matches 145; Conservative 74; Mismatches 281; Indels 215; Gaps 36;

QY 8 WASAGA-LALLAFAAQVTVPTVDLLANPPAGEWISYGOENRYRHSPLTQTTEWVG 66
Db 351 WIMPGTNALLSVQTQAD-----NNNAGD-----GOTHTGYNAGKMHYFRCTGQ 396

QY 67 LQJWARGMO---PGKQVYPLHDCVWMLANDGVYIAIDAKTGDLMEHRQLPNATL 129
 Db 397 MNINIQOGEINEJLKLITKVTGSNNQOFAADGTSSIOPI--KLNEIFLTKSN--NTAGL 452
 QY 125 NSFEGETR-----GMALYGTNVFV---SWDNHLVALDPAQOVFPDVRGGED 171
 Db 453 -KFGAPSOYDGTRTIQNMCGRTGEGQKNKVVIIKMGNSFNATGDRSEKREYFQVSDSGY 511
 QY 172 MYSNSGP-----IYANGVI-VAGSTCOYSPF---GCFVSGHD 205
 Db 512 FYAHRKAPTGETIGRIEAOFAADVAKGIANGFNRVVGSSALAGVWMSNGLFVGGG 571
 QY 206 SATGE-----ELMRN-----YFIRAGEGGETMGNDYFARMWIGAM 242
 Db 572 SITGVYKIGCTANALRIMAEYALFRSESENFYIIPNONEGES----- 616
 QY 243 GOI--TYDPVNLVHYGSTAVGPASETORGPGLTXGTNRF----- 283
 Db 617 GDHSLSRFPVRIGLNDGWVGLGRSOFIVDQNNALTTINSRRIANFRMQLQGSAYIDAE 676
 QY 284 ---AYRP-DTGTIVKRHOTLPBDNMDOCTEEMAVTVNDV-----QPSTEMEGLQST 331
 Db 677 CDDAVRPAGAGSFA-----SQNNEDVAPFPYMNIDRTDASAVYPLIKQRYVQNGCYSL 720
 QY 332 NFNAATGERRV-----LTGVPCKGTMMQOPDAETGERIAROTNYOMLESIDENG 382
 Db 731 GTLINNGNFRHYHGGNGSGTG-PQTADFGWEF-INGDFISPRDLIAKV--REDRIG 786
 QY 383 IVT-----VNEDALIKELDEYVVCPTFLGR--DWPSAALNDSGSIYFIPLNNVCYDM 434
 Db 787 NITGSGSGNFMNLNSTEST--KTDMSSYIPGAIPIPPS-----DS---VPAGFALMEG 835
 QY 435 MAVDOE-FTSMDYVTFNSVNTKLPPGKDMIGRIDALIDISTGRTLMSVF-----BAAN 485
 Db 836 QTFDSAPYKLAIVAPSGVIDPMGQITKRC-----PSGRAVLSEADGVKAKHSASAS 889
 QY 486 YSPVLT-----GGGVLFNGGIDRFPRALSQETGTLMOUOL 522
 Db 890 SSTDGTITTSFDPYGTKGTSTGCGTHSGSGSTJNGEHSHTIEMWN--GTVGCGNMK 946
 QY 523 ATVASGOAISYEVDMOYVALAGGVSYGSLNSALAGEVDSSTAIGNAVYFAL 577
 Db 947 ---SSYAISYRAGSN--TNAAGNHSHTFPSFGTSAGDHSVSGIAHHTHVAI 995
 RESULT 12
 US-08-322-760A-6
 Sequence 6, Application US/08322760A
 Patent No. 5877279
 GENERAL INFORMATION:
 APPLICANT: Goldberg, Edward B.
 TITLE OF INVENTION: MATERIALS FOR THE PRODUCTION OF
 NUMBER OF SEQUENCES: 6
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Pennie and Edmonds
 STREET: 1155 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: US
 ZIP: 10036
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/322,760A
 FILING DATE: 13-OCt-1994
 CLASSIFICATION: 530
 ATTORNEY/AGENT INFORMATION:
 NAME: Mistrock, S. Leslie

```

US-08-928-361B-30
; Sequence 30, Application US/08928361B
; Patent No. 6071518
; GENERAL INFORMATION:
; APPLICANT: Petersen, Carolyn
; TITLE OF INVENTION: PEPTIDES, POLYPEPTIDES, GLYCOPROTEINS,
; TITLE OF INVENTION: THEIR FUNCTIONAL MUTANTS, VARIANTS, ANALOGS AND FRAGMENTS
; TITLE OF INVENTION: FOR TREATMENT AND DETECTION/DIAGNOSIS OF CRYPTOSPORIDIUM
; TITLE OF INVENTION: SPECIES INFECTIONS
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PETERS, VERNY, JONES & BIRSA
; STREET: 385 Sherman Avenue, Suite 6
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306-1840
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/928,361B
; FILING DATE: 12-SEP-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/026,062
; FILING DATE: 13-SEP-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Verny, Hana
; REGISTRATION NUMBER: 30,518
; REFERENCE/DOCKET NUMBER: 480,76-1(HV)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-324-1677
; TELEFAX: 650-324-1678
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1043 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-928-361B-30

```

```

Query Match 3.5%; Score 108.5; DB 3; Length 1043;
Best Local Similarity 20.3%; Pred. No. 0.38;
Matches 141; Conservative 82; Mismatches 226; Indels 245; Gaps 39;

```

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QY 25 VTPYDELANPPAGEMISTYQONE-----NYRHSPLQITTEVNGQLVYARGMQ 77
DB 301 IDPTTG-LPENPPTGHLINPTNNMTDSSFAGAKYAVNSGKIDNV-----YGLPV 351
QY 78 GKVOVTPLIHGVNVLNAPGDVIOAIDAKTGDLIWEHRROLPNIAITNSFPTRGALY 137
DB 352 GEITGLP-----KDRGSDI-PFNSTIGELY-----DPSTGKPIN 384
QY 138 GTNAVYVSMNDHLVALDTATGQVTFVDYDRGGEDMANSNGPIYANGVYAGSTQYSPF 197
DB 385 NSTAGIVSGKRGKLPPIEDENGNTL-FD-----PSTNLPIDGNQLVNPET----- 427
QY 198 GCFVSGHDSAT-----GHELMRNKFIIP--RAGEGDETFWGDYDARMMTGAMQGITYPV 250
DB 428 NSTVSGSTGTTKRPKPGIPVAGGVVDEEAKDADK--GKD--GLIVPTNSINKDPV 482
QY 251 TNLVHYGSTA--VGPASETORGTPG-----GLYGTNTRFAVRP 287
DB 483 TNYQVSNNTGNINP--ETGKVIIGSLPGSLNYSFNPQOTDITLTKRPVDVTVGLPYDP 540
QY 288 DTGETVWRHQTLPNDN--WDQECTFEMMYTN-----VDVQ--PSTMEGIQS----- 330
DB 541 STGETIDPATKLPITPGSVAGDEILTEVLTITDEVTGLPIDLETGLPRDPVSGILPQLPNG 600

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QY 331 --INP-----NAATG---ERRVLTGVPKCTGT-MMQFD-----AETG 361
DB 601 TLVDPSSNKKPIPGSHSGFLNGTSGEQSHKDPSTKPLDPNPGGLRPDPBDSGLINPFG 660
QY 362 EFLMARDTNY-----QNMIESIDENGIVTVD-----DAI--- 391
DB 661 DLQSGHSTFMPVPKPGKENGIMTEPEQILDEAL--NKLPTSNVSNISPRSSDVAEDR 718
QY 392 -----LKEIDVEYD-----VCPTFLG--GRDMSAL--NPSGIYFILN 428
DB 719 PNTWMNKISGOTYVDGKRTIGSAASVIRHALLPTQDPTGLPSDPSTGLPIPGF 778
QY 429 NYCVDMAVDO-----EFTSMVNTSNVTKLPKDKMIGRIDAIDISTGRTIMSVERRA 483
DB 779 NVLVDPTQGEQIKGSVPVSLYVKEKNITVEAAYGL-----PYDPTKGPIDPI----- 827
QY 484 ANSPVYLTG-----GGVLFNGTIDRYFRA-----LSQETGETLMQT----- 520
DB 828 -SYLPPAKNGELIDPISGKVFSGSIAGISGRAGSQSKSDSGNPDIPSTMPYPKPG 886
QY 521 RLATVASGQAISEYDGMQYVALG-----GGV 548
DB 887 KLIDPESGAIIDNSVGV-FATVPGTAPKKGCV 919

```

RESULT 14

```

US-08-928-361B-6
; Sequence 6, Application US/08928361B
; Patent No. 6071518
; GENERAL INFORMATION:
; APPLICANT: Petersen, Carolyn
; TITLE OF INVENTION: PEPTIDES, POLYPEPTIDES, GLYCOPROTEINS,
; TITLE OF INVENTION: THEIR FUNCTIONAL MUTANTS, VARIANTS, ANALOGS AND FRAGMENTS
; TITLE OF INVENTION: FOR TREATMENT AND DETECTION/DIAGNOSIS OF CRYPTOSPORIDIUM
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PETERS, VERNY, JONES & BIRSA
; STREET: 385 Sherman Avenue, Suite 6
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306-1840
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/928,361B
; FILING DATE: 12-SEP-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/026,062
; FILING DATE: 13-SEP-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Verny, Hana
; REGISTRATION NUMBER: 30,518
; REFERENCE/DOCKET NUMBER: 480,76-1(HV)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-324-1677
; TELEFAX: 650-324-1678
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1721 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-928-361B-6

```

ADDRESS: PETERS, VERNY, JONES & BIRKS
STREET: 365 Sherman Avenue, Suite 6
City: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306-1840
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

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Db 827 ---SYLPPAKNGELIDPISGKYFSGSIAGFISGKAGSOSKSSDESGNPIDPSTNMPYDPK 883
OY 521 --RLATVASGOAISYEVDGMQYVAIAG-----GGV 548
 : | | | | | : : : | | |
Db 884 TGLIDPESGIAIDNSVSGV-FATVPGTAAPKKGCV 918

Search completed: August 8, 2001, 19:41:26
Job time: 83 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 8, 2001, 19:40:03 ; Search time 19.51 Seconds
(without alignments)
2260.639 Million cell updates/sec

Title: US-08-934-506a-5

Perfect score: 3089
Sequence: 1 MKPTSLMASAGALALLAAP.....GERVDSTAGNAVYFALPQ 579

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: PIR:68:*
2: PIR1:*
3: PIR2:*
4: PIR3:*
5: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	583	18.9	708	2 S52317	quinohemoprotein e
2	564.5	18.3	738	2 S14270	alcohol dehydrogen
3	561	18.2	742	2 A49340	alcohol dehydrogen
4	547.5	17.7	742	2 JS0326	alcohol dehydrogen
5	505	16.3	623	2 B83399	quinoprotein alcoh
6	468.5	15.2	626	2 JQ0706	alcohol dehydrogen
7	439.5	14.2	573	2 S68591	methanol dehydroge
8	392.5	12.7	796	1 JY0107	glucose dehydrogen
9	392.5	12.7	796	2 H85495	glucose dehydrogen
10	390	12.6	801	1 S00943	glucose dehydrogen
11	340	11.0	808	1 QPKEX	glucose dehydrogen
12	327	10.6	803	2 F83360	glucose dehydrogen
13	313.5	10.1	809	2 A55547	quinolate-shikimate
14	276.5	9.0	639	2 JC4881	polyvinyl-alcohol
15	221.5	7.2	221	2 A41378	hypothetical prote
16	167.5	5.4	407	2 H69064	serine/threonine p
17	167.5	5.4	524	2 A82580	polyvinylalcohol d
18	159.5	5.0	392	2 B85895	probable dehydroge
19	155.5	5.0	392	2 G65027	hypothetical prote
20	148.5	4.8	668	2 C75264	probable serine/th
21	145	4.7	1645	2 JN0896	crystalline surfac
22	142	4.6	943	2 JC4081	sucrase/fructanase
23	138.5	4.5	424	2 T29127	hypothetical prote
24	132.5	4.3	13055	2 T16580	hypothetical prote
25	132	4.3	407	2 C82804	conserved hypothet
26	128	4.1	1365	2 A41463	glucosyltransferas
27	126.5	4.1	5188	2 B85547	probable RTX fam11
28	126	4.1	613	2 F69424	conserved hypothet
29	126	4.1	955	2 G64866	probable membrane

30	124.5	4.0	1588	2 A86036	probable adhesin Z
31	122.5	4.0	547	2 H85699	partial probable a
32	122.5	4.0	644	1 I40712	endo-1,4-beta-xyla
33	122.5	4.0	799	2 T48889	serine/threonine p
34	122	3.9	386	2 A82284	conserved hypothet
35	121.5	3.9	603	2 F72237	conserved hypothet
36	121.5	3.9	827	2 F64512	hypothetical prote
37	121.5	3.9	1441	2 B86807	hypothetical prote
38	120.5	3.9	1197	2 D82696	conserved hypothet
39	120	3.9	380	2 C83171	hypothetical prote
40	120	3.9	746	2 B85557	coatomer complex b
41	119.5	3.9	796	2 T39862	erythronolide synt
42	119.5	3.9	3573	2 S23070	outer membrane por
43	119	3.9	443	2 S23771	Avicelase III - As
44	119	3.9	856	2 T00349	probable secreted
45	118.5	3.8	631	2 T35234	

ALIGNMENTS

RESULT 1

quinohemoprotein ethanol dehydrogenase (EC 1.1.99.-) type 1 precursor - Comamonas tes
C:Species: Comamonas testosteroni
C:Date: 08-May-1995 #sequence-revision 21-Jul-1995 #text-change 02-Jun-2000
C:Accession: S62366; S62373; S65908; S52317

R:Stoovogel, J.; Kraayveld, D.E.; van Sluis, C.A.; Jongejan, J.A.; de Vries, S.; Dui
Eur. J. Biochem. 235, 690-698, 1996

A:Title: Characterization of the gene encoding quinohemoprotein ethanol dehydrogenas
A:Reference number: S62366; MID:96184549

A:Accession: S62366
A:Status: preliminary
A:Molecule type: DNA

A:Residues: 1-708 <STOI>
A:Cross-references: EMBL:X81880; NID:g663195; PIDN:CA57464.1; PID:g663196

A:Accession: S62373
A:Status: preliminary
A:Molecule type: protein

A:Residues: 32-54 <STO2>
R:de Jong, G.A.H.; Geerlof, A.; Stoovogel, J.; Jongejan, J.A.; de Vries, S.; Duine,
Eur. J. Biochem. 230, 899-905, 1995

A:Title: Quinohemoprotein ethanol dehydrogenase from Comamonas testosteroni. Purific
A:Reference number: S65908; MID:95324580

A:Accession: S65908
A:Molecule type: protein
A:Residues: 32-50, 'X', 52-54; 477-483, 'X', 485-490 <DEJ>

A:Experimental source: ATCC 15667
C:Genetics:

A:Gene: qhdh
C:Superfamily: glucose dehydrogenase (pyrroloquinoline-quinone)
C:Keywords: oxidoreductase; quinoprotein

F:1-31/Domain: signal sequence #status predicted <SIG>
F:32-708/Product: quinohemoprotein ethanol dehydrogenase type 1 #status experimental

Query Match 18.9% Score 583; DB 2; Length 708;
Best Local Similarity 27.9%; Pred. No. 1,3e-32;
Matches 173; Conservative 95; Mismatches 271; Indels 82; Gaps 22;

QY	3	PTSLMASAGALALLAAPFAQVTPVT-----DELLANP-AGEMISYGNQEN 50
DB	12	PERMWMILAACG--SAAFAQTGPAQAQAAAVORVDGDFIRANAARTPMPPTIGVDYAE 69
QY	51	YHSPETOTTENNVOLOLVAKRMQPK-VQVTPLIHDGVYLANGVYQIAIDAKTCD 109
DB	70	TPYSRIDOINAAVNDLGLAMSYNLESTRGEATPVVVDGIMYSASMSVYHAIDRTGN 129
QY	110	LMEHRROLPNATLNSPGE-PTRGMALYGTNVYFVSNDMLVALDTATG-----QVTFD 163
DB	130	RIMYTDPOIDRTGKGGCDVYVNRGVALLMKGVYVAGAMDGLIALDAATGKEVHWHTFE 189
QY	164	VDRGGEEDMWSNSGPVYANGVYAGST-CQYSPRGCVSGHDSATGEELMRNFIP--- 219

RESULT 2
S14270
alcohol dehydrogenase, membrane-bound (EC 1.1.-.-) 72k chain precursor - Acetobacter
C:Species: Acetobacter polyoxogenes
A:Valley: Strain NB11028
C:Date: 21-Nov-1993 #sequence,revision 26-Jul-1996 #text_change 20-Jun-2000
C:Accession: S14270
R:Tamaki, T.; Fukaya, M.; Takemura, H.; Tayama, K.; Okumura, H.; Kawamura, Y.; Nishiyama
Biochem. Biophys. Acta 1088, 292-300, 1991
A:Title: Cloning and sequencing of the gene cluster encoding two subunits of membrane-
A:Reference number: S14270; MUID:91155482
A:Accession: S14270
A:Molecule type: DNA
A:Residues: 1-738 <TAM>
A:Cross-references: GB:00635; NID:g216185; PID:BA00528.1; PID:g216186
A:Experimental source: strain NB11028
C:Complex: heterodimer of 72k and 44k chains
C:Superfamily: glucose dehydrogenase (pyrroloquinoline-quinone)
C:Keywords: alcohol metabolism; membrane protein; oxidoreductase
E:1-35/Domain: signal sequence #status predicted <Sig>
F:36-78/Product: alcohol dehydrogenase 72k chain #status predicted <NAT>

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Db 197 TYDGAIRIANGVILICN - GGSEEGARGVFSAPDAETGKVDHREFFVYVNPKNPEDDAASD 254
QY 227 -----ETWGNDEYEARMTGA-----WGQITDYPVNLVHYGSTAVGASSETOR 269
Db 255 VLMKNAVQTS-----PTGAWTROGGGGTVDMSIYDVPVADVLVGYNGSNPNMYKXR 307
QY 270 GTPGGVLLYGNTREFAVRPDGEIYVNRHQLLPRKNNMOQCTFEEMAVTNVDVQSTEMEGLQ 329
Db 308 SEEGGNLLEGSIVALKPETGEYVNHFOETPMOOWFETSDOOIMTLDLPI----- 357
QY 330 SINPNATGERRVLTVGPCKTGTMMOQDAETGEFEALDARNYQNMIESID-ENGIVTYNE 388
Db 358 -----NGETRRVYIYHAKNGEFFYIIDAKTGEELSGKNYVYVMAAGSDPPGTGRPIYNP 410
QY 389 DALIKELDEYDVCPEFLGGRDMPSPALNPDGSIYFIPLNNVCYDMAVADQEFF-SMDY 447
Db 411 DALYLTLTGKEMVGIPEDLGGHNPAAAMAFSPKXGVIYIPAOVPELITNOVGCFTHPBDM 470
QY 448 NTS---NYTKLPPG-----KDMIGRIDAIDISTGRTLSVERAANYSPVLSTGGCV 496
Db 471 NGGLDMNKKGIPDSEAKQAFVKDLKGWIVADMPQKQAEAMRHVDHKHPNGGILATGGDL 530
QY 497 LPPGGDRFRALSOETGETLMOYTRATAYASQALSIYEDVGGQYVYAIAG 546
Db 531 LFQGLANGBEHAYDATNGSDLFHAADSGIILAPPTYLANGQYVYAAVEGG 580

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Query Match	18.2%	Score 561;	DB 2;	Length 742;
Best Local Similarity	28.5%	Pred. No. 4,6e-31;		
Matches 173;	Conservative	90;	Mismatches 248;	Indels 96;
			Gaps 21;	
11	AGALMLAAPAAQVTPVDEL--ANPPAGEMISYGCNGQENYRHSPLTQITENWGLQ	68		
23	AAALPFAAIPARADQGMTGEALIHADHPENMLSTGYTSEQKYSPLDQINRSNVCDLK	82		
69	LYWAGMGQPGKQV-VTPRLIHGVMILANPGVIOAIDAKTGDLIWEHRRLDP-NIATLNS	126		
83	LAWYTLTDTNRQEAFTPLVVDGIMVATTNWSKEMALDAATGKLMQYDPRKGVGNIADKGC	142		
127	FGEPTRGMALXGTNYVEFSWMDNHLVALDPTATGQVTFDV-----DRGCGEDWSSNSGPI-	180		
143	CDTVNRGAGYNNKGVFWGTFDGLVLVADAKGKKVMEVNTIPDASLGRQSRSTVDCAVR	202		
181	VANGIVAGSTICQVSPFEC--FVSGHDSATGEEELMKRYFTIPRAGEGD-----	226		
203	VAKGIVLLIGN--GSGEEGARGFVSAPFAETGKLMKREYTPVNNKNEPDHNVADNVLMASKA	260		
227	ETWGNDEYEAQMNT-----GAMQITVDPTVNLVHGYSTAVGPASETQRTPGCTLY---	277		
261	YKTMGP--KGAMVROGGGVTWDSLVDVPSDLV---LAVG-----NSPPNNYKTRSE	309		
278	--GNN---TFEAVRPDTGELIYVNHQTLPRDNDQECTFEMAVTIVNDVDPSTMEGLQSI	311		
310	GIGSMFLGSLVALKPEETGEVYWHFQATPMDQMDYTSVQDINTLDMFV-----	357		

```
QY      332 NPNMATEG-RKVLIVGPOCKTGMNQFDEAGTEGLMARNTYNÖNNIESTE-NGIVTVNED 389
        || | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      358 -----NGEMRHVIMHAP-KNGFFYLDAKTGEELAGKKYTYÖNNANGLDPLTGRIINPD 411
        || | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY      390 AILKELDEVYVCPTFLGGRWPSAALNPDSGIYFIPLNNVCY-----DMAA 436
        || | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      412 GLYTLCKEFWYGIPICGAHNFMGMAYSPKTHLYLVLPKHQITPEFGYKNVGFKPHDPAMN 471
        || | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY      437 VDQETSMADVNTINSVTKLPRPKMDIGRIDALIDISTGTSLMSVEREAANTSPVLSTGGGV 496
        : | : : | : : | : : | : : | : : | : : | : : | : : | : : |
Db      472 VGLDTNKGLPDTPE-AATYAIKIDLHGWLAMDVPYKMTVWKIDIKGWNSGYLATGGDL 530
        : | : : | : : | : : | : : | : : | : : | : : | : : | : : |
QY      497 IENGCTDIRFRALSOETGETLMOTRLATVASQAQLSYEVNDQMÖYA-----TAGG 546
        || | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      531 LFOGLANGEFHAHDATNAGSDLYKFDAQSGIIASPMWTYSVNGKOYAAVEVMGGLYPIISMG 590
        || | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY      547 GVSYSYG 553
        || | | | |
Db      591 GVGRTSg 597
```

RESULT 4
 JS0326
 alcohol dehydrogenase (EC 1.1.-.-) 72k chain precursor - Acetobacter aceti
 C:Species: Acetobacter aceti
 C:Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 20-Jun-2000
 C:Accession: JS0326
 R:Inoue, T.; Sunagawa, M.; Mori, A.; Imai, C.; Fukuda, M.; Takagi, M.; Yano, K.
 J. Bacteriol. 171, 3115-3122, 1989
 A:Title: Cloning and sequencing of the gene encoding the 72-kilodalton dehydrogenase sub
 A:Reference number: JS0326; MUID:89255070
 A:Accession: JS0326
 A:Molecule type: DNA
 A:Residues: 1-742 <INO>
 A:Cross-references: GB:D90004; GB:M26951; NID:g216193; PIDN:BAAL4058.1; PID:g216194
 A:Experimental source: strain K6033
 A:Note: amino terminal of mature protein is confirmed
 C:Genetics:
 A:Gene: adh1
 C:Superfamily: glucose dehydrogenase (pyrroloquinoline-quinone)
 C:Keywords: alcohol metabolism; NAD; oxidoreductase
 F:1-35/Domain: signal sequence #status predicted <SIG>
 F:36-742/Product: alcohol dehydrogenase 72k dehydrogenase chain #status predicted <ADC>

[illegible]

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OY      NPNNATGG--REVVLVGPOCKTGTMMOQFDEATSEFLPMARDINTYNONNIESID-----EN 381
Db      -----GEMRHVHYHAP-KNGFFYLDAKTISEFLSGKNYYVQNMANGGLDPLTGPRMYPND 411
OY      GIVTVNEDEAIILKELDVEYDVCPTEFLGGRDPWSAALNPDSGIYFIPLPANCY----- 432
Db      GLYTLLG-----KFWYGI-PCGPLAHNFAMAMAYSPTKLHVYTPAQIDIPGYKNOVGF 463
OY      ----DMAAVDDSEFTSMVDYNTSVNTKLPPCGKDMIGRIDAIDISTGRTLMSVERAAANTSP 488
Db      KPHASISNVNGIDMTKNGI.PDTPE-AKTAYIKDLHGWLAMPVYMETWYWKIDHKGPWNNG 522
OY      VLSITGGVVLFGNGIDRYFRALSQETGETLMOTRLATYASGAALISEYDGMQYA----- 542
Db      ILATGSDILLFOGLIAGDEFHADVATNGSDLYKFEDAOSSIIAPMPYVSNGKYOVAEYWG 582
OY      -----TAGGVSYSGSL-----NSALAGERVDSRA 567
Db      GIYPIISMGGVGRTSGWTYNHSTIALEFLDGKA 614
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RESULT 5
B63399
guinoprotein alcohol dehydrogenase PA1982 [imported] - *Pseudomonas aeruginosa* (strain
C:Species: *Pseudomonas aeruginosa*
C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C:Accession: B63399
R:Stover, C.K.; Pham, X.O.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.;
adaman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Lardig, K.; L
..; Lorry, S.; Olson, M.V.
N:ature 406, 959-964, 2000
A:Title: Complete genome sequence of *Pseudomonas aeruginosa* PA01, an opportunistic pathogen
A:Reference number: A82950; MUID:20437337
A:Accession: B63399
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-623 <STO>
A:Cross-references: GB:AE004624; GB:AE004091; NID:g9947973; PIDN:AAG05370.1; GSPDB:GN
A:Experimental source: strain PA01
C:Genetics:
A:Gene: exaA, PA1982

Query Match	16.3%;	Score 505;	DB 2;	Length 623;
Best Local Similarity	25.7%;	Pred. No.2.7e-27;		
Matches 164;	Conservative 105;	Mismatches 276;	Indels 92;	Gaps 23;
QY	3	PTSLIWMASGALAL---	LAAPFAQVTPYTDLLAN--	PPAGEMISYCONOEYRHSPLT 57
Db	9	PAGILRPSLHCLAF	AVALSAGALAKDVTMEDIANDDKTTGVDLYOGAGTAAQRKSP	LK 68
QY	58	QITTEVNGOLUWARGM----	OPRKVQVPLTHDGVMYLAN	PGVLIQAIDAKTGLDWE 113
Db	69	QVADNADNFKLTPMAW	MSIFGDEKORQ--	ESALYSDEVIYYTASYSFLFALDAKTGRRLMT 127
QY	114	HRHQLP-----	IATINSFGEPTRGALYGTNY	EVYSMDNHLVALDPTANGQTFD--VD 165
Db	128	YNHRLPDDITRCCDVAN-----	RGAALYGDYKFEFTGLDASVAL	LNKNTGKYVKKKKFAD 181
QY	166	RGQGEDMVAWSSGPIVANG----	VIVAGSTCOYSPRCF--	VSGHDSATGEELMKNFYI 218
Db	182	HGAGYTM--TGAP	LIYVADKTKGKVLHIGSS--	GDEGGVYGRFLFADPDPTEGEEIWMRPVY 237
QY	219	PR-----	AGEEGDETWGNDYEA-----	KMTGCA---WQIYYDPTNLYNHG 257
Db	238	EGHMGRLNGKSDIYTG	GVKAPSWPDDRNSTPGKVES	SHSGGAPWQASASDAETNIIYVG 297
QY	258	STAVGPAASEFQKGPFG----	TLVGTNTRFAVVRPDTGEI	YVHRHDTLPDNDNDQCFEE 311
Db	298	AGNGCPMNNTAKRAKGA	GNPNHDIYDLY--TSQ	OVGDPSSGEVKKFNYQTTPNDANDPFGNNE 356
QY	312	MMTNTNVQVSTMEKGIQSINP-----	AATGERRRVLTVPC	KTGTMW--QFDAETGEEL 364

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Db 357 LVLEFYKKKDKIVKATAHADRNNGFFIYVVDNSNGKIQNAFPFVDNTTASHIIDTKTG--- 413
QY 365 WARDNTYONMIESIDENGIVTVNEDALIKELDEVYDCPTLGGHWPSSALNPDGSIYE 424
Db 414 --RPVERGGORPPLPEPG-----QKHGKAVEGSPPLPGKNNMPPMAYSDQDTGLFY 461
QY 425 IPLNVGCDMAVADDEFMSMDVYNNTNTKLPCKDMIGRIDALDISTGRTLSVERAAA 484
Db 462 VPANMKEDYITTEESYTKGSAYLGMGRIRKMYDDHVSGLRADDPVSGKVVMEHKEHLP 521
QY 485 NYSPLSTGGVLFNGGDRYFRALSOFTGETLMOTRLATYVAGSAISYEVDMQYVAA 544
Db 522 LMAGVLATAGNLVFTGTGDGYEFKAFDAKSKGELMKFPQGSIVSPPLTMEDEGQIYGV 581
QY 545 GGGVSYSGSLNALSALGERVDSST---AIGNAVYVRLP 578
Db 582 ---VGYG-GAVPLMGDMADLTRPVAOGGSPFWFKLP 614

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RESULT 6

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J00706
alcohol dehydrogenase (acceptor) (EC 1.1.99.8) alpha chain precursor - Methyllobacterium
N:Alternate names: methanol dehydrogenase 62K large chain
C:Species: Methyllobacterium extorquens
C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 08-Oct-1999
C:Accession: J00706; S07908
R:Anderson, D.J.; Morris, C.J.; Nunn, D.N.; Anthony, C.; Lidstrom, M.E.
Gene 90, 173-176, 1990
A:Title: Nucleotide sequence of the Methyllobacterium extorquens AM1 moxP and moxJ genes
A:Reference number: J00706; M0ID:90337342
A:Accession: J00706
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-626 <AND>
A:Cross-references: GB:M31108; NID:g150017; PIDN:AAA25380.1; PID:g150018
A:Experimental source: strain AM1
R:Nunn, D.N.; Day, D.; Anthony, C.
Biochem. J. 260, 857-862, 1989
A:Title: The second subunit of methanol dehydrogenase of Methyllobacterium extorquens AM1
A:Reference number: S04644; M0ID:89350892
A:Accession: S07908
A:Molecule type: protein
A:Residues: 28-50, 'XX', '53' <NUN>
A:Note: the source is designated as Methyllobacterium extorquens AM1
C:Comment: This enzyme oxidizes methanol to formaldehyde.
C:Genetics: moxP
A:Gene: moxP
C:Keywords: alcohol metabolism; oxidoreductase
F:1-27/Domain: signal sequence #status predicted <SIG>
F:28-626/Product: alcohol dehydrogenase (acceptor) #status experimental <MAT>

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Query Match 15.2% Score 468.5; DB 2; Length 626;
Best Local Similarity 25.4%; Pred. No. 9.3e-25;

Matches 159; Conservative 113; Mismatches 271; Indels 83; Gaps 23;

```

QY 10 SACALALLA-AP-AFAQVPTVDELINPAGE-WISYQONENYHSPLOITTEWNGO 66
Db 7 SYSALAMALAPALSSAYANDKVELSKSDNNWMPKNTSDNNFSLKQINKGNKQ 66
QY 67 LQLYW--ANGMOGKQVTPPLIHGVMYV--ANPGVDIQAIDAKTGDLIWEHR-RQLPNI 121
Db 67 LRPAMTFSTGLNGH-EGAPLIVVDGKMYIHTSPNNTFALGDDPGTILMOQKPKQNPA 125
QY 122 ATLSNFGPTRCMALYGTN-----VYFVSMNHLVALDTAGQVTFEYDRGQGDWNSN 175
Db 126 KAVACCDLVNRLGATYPPCGKTPALLKTLQTDGNVAALNAETGVTWKEVNSDIKVGSTL 185
QY 176 SSGPIYANGVIVAGSTQYSPFCFVSGHDSATGEELMKNFYI-----P 219
Db 186 TIAPYVKKDKVIIGSSGALGVRLTAVDVKTGEQWRAVATGPKDKLLASDENINAP 245

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QY 220 RAGEE--GDETWGNDYEARMGTGA---WGQITPDYTNLVHYGSTAVGPASGTQGTGG 274
Db 246 HYCKGIGTGTWEGD---AMKIGGTMNGWYAYDPCTNLITFOTGNPAPNEMNR--PBD 300
QY 275 TLVGTNRFPAVRPDGTGIWRRHOTLRDNDQDCTEEMAMTVNDVQPSYEMEGLOSINP 334
Db 301 NKW-TMTIFGRDADTGEAKGYOKTPHDEWD-----YAGVNVMMISEOKD----- 344
QY 335 AATGERVLTGVPCKTGTMMQFPAETGEFLMAR---DTYONMIESIDENGIVTVNEDA 391
Db 345 -KDGKARKLLTHDRNGIYTLIDRTGALYSANKLDDT--VAVFSVDLKTQOPVAPDEY 401
QY 392 LKELD-VEIDVCEPTLIGRDPWPSALNPDGSIYEIPLNNVCYDMAVADDEFMSMDVNTS 450
Db 402 GTMDHLAKDICPSAMGYNHOCHSDYPRRELFEMGINICHIMDEPFLPRAQGFVGA 461
QY 451 NVTKLPPGK-----DMIGRIDAIDISTGRTLSVERAANSPILSTGGVLFNGGDR 504
Db 462 TLNNYPPGPKDGRQNYEGLOIKAYNAITGDIYKMKERFAVNGTMAAGDLVFGTLDG 521
QY 505 YFRALSQETGETLMOTRLATYVAGSAISYEVDMQYVAI---AGGGSYSG-----S 552
Db 522 YLKARSDPTGDLIMKFKIPSGAIGYPMYTHKGTQYVALYVGGMPGVLFDLADPTA 581
QY 553 GLNSALAGERV-DSTAIQNAVYVRLP 577
Db 582 GLGAVGAFKRLANNYTMGGGVVYFSL 607

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RESULT 7

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S68591
methanol dehydrogenase (EC 1.1.1.244) heavy chain - Methylotrophus methylotrophus (str
C:Species: Methylotrophus methylotrophus
A:Variety: strain W3A1
C:Date: 06-Dec-1996 #sequence_revision 13-Mar-1997 #text_change 08-Oct-1999
C:Accession: S68591
R:Xia, Z.; Dai, W.; Zhang, Y.; White, S.A.; Boyd, G.D.; Mathews, F.S.
J. Mol. Biol. 259, 480-501, 1996
A:Title: Determination of the gene sequence and the three-dimensional structure at 2.
A:Reference number: S68591; M0ID:96256524
A:Accession: S68591
A:Status: Preliminary; nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 1-573 <XIA>
A:Cross-references: EMBL:U04040; NID:g1127819; PIDN:AAA83765.1; PID:g1127820
A:Note: the authors did not translate the codons for residues 1-2
C:Keywords: oxidoreductase

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Query Match 14.2% Score 439.5; DB 2; Length 573;
Best Local Similarity 24.5%; Pred. No. 8.4e-23;

Matches 146; Conservative 99; Mismatches 259; Indels 93; Gaps 21;

```

QY 38 AGEWISYQONENYHSPLOITTEWNGOQLVW--ARGMOGKQVTPPLIHGVMYV-- 93
Db 13 AGAMPILATGGYYSQHNPSLAQINKSNVKNKAWSFTGVLNGH-EGAPLIVIGDMNVHS 71
QY 94 ANPGVDIQAIDAKTGDLIWEHR-RQLPNIATLSFGEPTGMAIYGNVYFVSMNHLVA 152
Db 72 AFPNNYVALNLDGKTIWQHPRKODASTRAVMCCDVADVGLAYGAQIYKQANGHLLA 131
QY 153 LDTATGQVTFEYDRGQGDWNSNGSPIVANGVIVAGSTQYSPFC--FVSGHDSATGE 210
Db 132 IDAKTGKINWEVCECDPKVSGSTLQAPFVAKDVLYLKG--CSGAEGLGVRAVNAFIDLKTE 189
QY 211 ELWR-----NYFIPRAGE--EGDETWGNDYEARMGTGA---WGQITYPD 249
Db 190 LKWRAPATGSDSVYRLAKDFNSANPHYGGGLGKTMWEG--AMKIGGTTMNGWAIYDP 246
QY 250 VTNIVHGSTAVGASGTQGTGG-----TLVGTNRFPAVRPDGTGIWRRHOTLRDND 304
Db 247 KLNLFYSGNPAFNMETMR--PDKNKMTMTIMGRLD-----DTGMAKWGYOKTPHDEW 298

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Db 593 -----VPPGMLGVFENGCMGVNPDROVAVANNPITGLPFVSRLLIPADPNRAQTAK 641
 Qy 426 -----PLNNVCYDMAVDEFTSMDEVNTSNVTKLPPGKDMIGRIDADISTGRILM 477
 Db 642 AGTEGCVQPMGVVY-----GVEISAFSLPLGLPCPKPAMQYVAGVDLKTREVVW 691
 Qy 478 -----SVERAAANYSPVLSTGGGVLFNGST-DREYFALSOEGETILM 518
 Db 692 KKRIGTIRDSLPNLFQLPVAKIGVPLGSGISTAGVNVFVAGQODVYLAENVTKKILM 751
 Qy 519 QTRLATVASGA--ISYEVDMQYVAI-AGGGVSYSGSLNSALAGERVSTAIGNAVYF 575
 Db 752 EALPL-AGGQATPMTEYELNGKQYVIMAGGHSFG-----TKMGDYLAVX 795
 Qy 576 ALP 578
 Db 796 ALP 798

RESULT 11

QPKEX
 glucose dehydrogenase (pyrroloquinoline-quinone) (EC 1.1.99.17) - Glucobacter oxydans
 C:Species: Glucobacter oxydans
 C>Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 22-May-1998
 C:Accession: S17716; S19265
 R:Cleton-Jansen, A.M.; Dekker, S.; van de Putte, P.; Goosen, N.
 Mol. Gen. Genet. 229, 206-212, 1991
 A:Title: A single amino acid substitution changes the substrate specificity of quinoprot
 A:Reference number: S17716; MUID:92017653
 A:Accession: S17716
 A:Molecule type: DNA
 A:Residues: 1-808 <CLE>
 A:Cross-references: EMBL:X62710
 R:Goosen, N.
 submitted to the EMBL Data Library, February 1992
 A:Reference number: S19265
 A:Accession: S19265
 A:Molecule type: DNA
 A:Residues: 1-212 'A', 214-808 <GOO>
 A:Cross-references: EMBL:X62710; NID:958416; PID:958417
 C:Genetics:
 A:Gene: gdh
 A:Function:
 A:Description: catalyzes the oxidation of D-glucose to D-gluconic acid by ubiquinone
 A:Pathway: respiratory chain
 C:Superfamily: glucose dehydrogenase (pyrroloquinoline-quinone)
 C:Keywords: oxidoreductase; pyrroloquinoline quinone; respiratory chain; transmembrane P
 F:9-28/Domain: transmembrane #status predicted <TM1>
 F:35-54/Domain: transmembrane #status predicted <TM2>
 F:60-76/Domain: transmembrane #status predicted <TM3>
 F:94-110/Domain: transmembrane #status predicted <TM4>
 F:122-138/Domain: transmembrane #status predicted <TM5>
 F:91/93/Binding site: ubiquinone (Air, Asp) #status predicted
 F:470/Active site: Asp #status predicted

Query Match 11.0%; Score 340; DB 1; Length 808;
 Best local Similarity 21.8%; Pred. No. 1,1e-15;

Matches 159; Conservative 98; Mismatches 259; Indels 212; Gaps 30;

Qy 13 ALALLAFAFAQVPTVDLELA-----NPPAGEWISYGONENYRHSPLTQIT 61
 Db 128 AVLALFASLFDPPDISGLPTQIANSPADPNVPASEMHAYGRTOAGRWSPILQINA 187
 Qy 62 ENVGQQLVW-----ARKQPGKV-QVTPLLHDGVMYLANGVDTIOAIDATGDLIW 112
 Db 188 TNSVNLKAVAMHITKDMNNSNDPEQINEATPIEFNNLTLYMCSLHQKLEAVDGAATGVNKM 247
 Qy 113 EHRRL-----PNIATLN-----SFGG-PTFGMALYGT-----NYFVSWDNHVALDT 155
 Db 248 YDPRKLTQINPFGHILTCGYSFHEHPANAMSDGNPAPTDCAKSLIPVN-DGRLEVEDA 306
 Qy 156 ATGVTFDV-DRGGEDMVSN-----SSGPIYANGVYA-----GSTCQYSP 196

Db 307 DTGKTCGFGNNGEIDLKVPNQPTTFPGQYEPTSPVITDKLILANSALIDNCSVKQASG 366
 Qy 197 FCGVSGSDASTGTELM-----RNFIFRAGEGDETNQNDVFAAMTQAMQIYDPTVN 252
 Db 367 --ATQAFDVTYGRKRWVFDSANPDNQLPDESHPVFHPNSPNWISY-----SYDANLN 418
 Qy 253 LVHVGSTAVGASFTQKTP---GGTLYGTNTRF-----AVRPDTGELIWRHQTLPRDNW 304
 Db 419 LVYIPMGV-----CTPDQMGDRTRKDSERFAPGIVALNADTGLKAMPYQVHHDLW 469
 Qy 305 DQCTFEEMVTVNDVQSTEMEGLQSLNPNAATGERRLVTPCKTGTMMQFDETG-EF 363
 Db 470 DMELPSQPSLVDTQKQDGLVPAIYA-----PKTGDIFFLDRTGKEI 513
 Qy 364 LMARDT-----NYQNMIESIDENGIVTVNEDALIKELDY----- 397
 Db 514 VPAPETPVQGAAPGDHNSPTQPMSSO---LTLRKPNLNSDDINGGTFIDQMFCSYFHT 570
 Qy 398 -EYD-----VCPTEFGGRDMPSAALNPDGCIYFIPLNNVCYDMAVDO----- 439
 Db 571 LRYEGPTTPSLKSLIFRPDGLMFEWGLAVDPQROVAFANPISLPSVQLVFRGPNP 630
 Qy 440 -----EFTSMDEVNTSNVTKLPPGKDM-----GRIDAIDIST 472
 Db 631 IMPERNAKGTGETGLQHNHYGLPVAVNLHPFLDVLLEFGIKMPCRPWPWGVAGIDILKT 690
 Qy 473 GRTLVSEBAANYS-----PV-----LSTGGGLV-F-NGSTDYFRALS 510
 Db 691 NKVVQHRNGTIRDSMYGSSSLPPLPIRKIGVPSLGGFLSTAGNIGFLTAMDYIRAYN 750
 Qy 511 QETGETLMQTRLATVASGOAISYEVDMQYVAIAGGVSYSGSLNSALAGERVSTAIGN 570
 Db 751 LTTGKVLWMDRLPAGAQTPTTYAINKQYI-----VTYAGGHSNF-----PTRMGD 797
 Qy 571 AVYVFLAP 578
 Db 798 DITAYALP 805

RESULT 12

F83360
 glucose dehydrogenase PA2290 [imported] - Pseudomonas aeruginosa (strain PA01)
 C:Species: Pseudomonas aeruginosa
 C>Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
 C:Accession: F83360
 R:Stover, C.K.; Pham, X.O.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.;
 Adam, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; L
 .; Lory, S.; Olson, M.V.
 Nature 406, 959-964, 2000
 A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pa
 A:Reference number: A82950; MUID:20437337
 A:Accession: F83360
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-803 <STO>
 A:Cross-references: GB:AE004654; GB:AE004091; NID:99948311; PIDN:AA605678.1; GSPDB:GN
 A:Experimental source: strain PA01
 C:Genetics:
 A:Gene: gdh
 C:superfamily: glucose dehydrogenase (pyrroloquinoline-quinone)

Query Match 10.6%; Score 327; DB 2; Length 803;
 Best local Similarity 21.9%; Pred. No. 8,6e-15;

Matches 166; Conservative 84; Mismatches 265; Indels 244; Gaps 32;

Qy 6 LLM-----ASGALALLAFAFAQVPTVDLELANP----- 36
 Db 103 LLMVPMFRRLADGAPALGTALGVAVVLAGAAAGSO-FTNPGQIVGRIDRDSGMTST 161
 Qy 37 ----PAGEWISYGONENYRHSPLTQITTEVNGQLDLMVARGMQPGKV-----Q 81

Db 162 APAMPDGMQAYGRTEFGDRYSPLKQITPANVQGLEEAMR--IRTDGLPTADPLELTNE 219
 QY 82 VTPLIHGVWYLANPGVIOAIDAKTGDLIMEHROPLNATLNSFGEPT- RGMALYGTN 140
 Db 220 NTFPLKVMGLACTAHSAHSLADLPDGTGAELMRPDQIQSPVGEKGFAMHMCRCGVSYDEE 279
 QY 141 VY-----FVSWDNHLVALDTATGCV-----TFDV 164
 Db 280 QYASDVGAPPAALSEAGKAAVASCPRRLFLPTADARLAIAMNGKVCDFGKGAVDL 339
 QY 165 DRGGE---DMVNSSPPIYANGVIYAG---STCOYSPGCFVSGHDSATGEIMRNY 216
 Db 340 TAGIGPTPGGYSTSPAAYTRNLVIGHVTDNESTNEPSG-VIRAFDVHDKLVW-NM 397
 QY 217 FIPRAGEGDETWGNDYEARMTCAMGQITVDPYTNLVHGSTAVGASSTORG---TPG 273
 Db 398 DSGNDPEELAPKRY-TRNSPMMMSLASVDEKLGQY--LPLGQMPDQMGNTPG 453
 QY 274 GTLYGTNTRFAVRPDTEIYWRHQTLPRDWMDOCTPEMMVTNVQVPTSTEMEGLQSI 333
 Db 454 AEKFSAGL-VALDLNTGKLRNVOFTHDLMDM-----VGSQPTL-----LDL 496
 QY 334 NAATGERVLTGVPCCKTGMQPDATG----- 361
 Db 497 KTADGVAPALI-AFTKQGLYLVDLRDGTPIVPIREVPAGAVEGDHTAPQARSDNL 555
 QY 362 -----EPLMA-----RDTNYQNMIESIDENGIVTNEDALTKELDYEDY 401
 Db 556 LRPLTERDMWSSPFDQMLCRIOFSLRYEGQYTPPSEGS- 599
 QY 402 CPPLFLGRDMPASALNDSGIYFPLNNVCYDMAAVDOEFT---SMDVNTSNVTK- 454
 Db 600 YPGNVGVFNMGVSVDPVRQILFTSPNYMAFVGQWPRDKVPSGRREGTSCVQNTGA 659
 QY 455 -----LPGKMIGRIDAIDISGRTILMSVERAA-HYSPY----- 489
 Db 660 PYAVIMHPFSPISGLPQAPSWCDVAGIDLTTAKVWQHNGTSRNTPTPIGLTVGVPS 719
 QY 490 -----LSTGGVLENGGT-DRYFRALSOETGELTMOTRLATVASQA--LSYE-VDGMOYV 541
 Db 720 MGGSITTAGVAFPLSGTLQDLARAYVKOSKOLQARLP--AGQATPPSYTKDKRQYV 777
 QY 542 AIVAGGCVISGSLNSALAGERVDSALGNAYVYFALPQ 579
 Db 778 LIVAGGHRGSPG-----TRMGDIYALVALPR 802

RESULT 13

A55547
 quininate-shikimate dehydrogenase (EC 1.1.99.-) - Acinetobacter calcoaceticus
 C:Species: Acinetobacter calcoaceticus
 C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 26-Aug-1999
 C:Accession: A55547
 R:Elasmere, D.A.; Ornstom, L.N.
 J: Bacteriol. 176, 7659-7666, 1994
 A:Title: The pca-pob supraoperonic cluster of Acinetobacter calcoaceticus contains glnA.
 A:Reference number: A55547; MUID:95095936
 A:Accession: A55547
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-809 <EIS>
 A:Cross-references: GB:U1154; NID:9508824; PID:9508825
 C:Genetics:
 A:Gene: glnA
 C:Superfamily: glucose dehydrogenase (pyrroloquinoline-quinone)
 C:Keywords: membrane protein; oxidoreductase

Query Match 10.1%; Score 313.5; DB 2; Length 809;
 Best Local Similarity 23.3%; Pred. No. 7.5e-14;
 Matches 160; Conservative 80; Mismatches 262; Indels 185; Gaps 26;

QY 3 PPSLWASGALALLAA-PAFAQVTPVDELLANPAGEMISYGNQENYRHSPLTQITTT 61

Db 148 PHETVAAAGEELPLVVDPAKKOV-----NWDHYGNDAGSRFVALDQINR 193
 QY 62 ENVGQOLVW-----ARGMQPG-KVQYTPLIHGVWYLANPGVIOAIDAKTGDLIME 113
 Db 194 NNYSKLKEAMRFRTGDFLTGTGGAEDQMTPLQVGNKVFELCPHNHNTAIDDSQKLMK 253
 QY 114 HRROLPNATLNSFG---EPTRGMALYGT-----NYFV 144
 Db 254 -----AEVNSTADAMERCGRVAFDSTOPLVQPTLAGATPVAALANTECPRRVYTN 305
 QY 145 SWDNHLVALDTATG-----QVFEDVDGQGEDVNS-----SSGPIYANGVIYAGSTC 192
 Db 306 TYDGRILAVNADTGACRCPYNGVYNLHEGIGENTKAPREYVTAAPITAGTIYVGSRI 365
 QY 193 QYSPF---GCFVSGHDSATGEELMRNYFIPRAGEGDETWGNDYEARMTCAMQITVD 248
 Db 366 ADVNADMPGVIYRAVDYTTGKLHMA--FDPANPDPNVYLRKGEIYKRSSSTSMAMASYD 423
 QY 249 PVTNLVH--YGSTAVGASETQRTPGTLGTNTRFAVRPDTEIYWRHQTLPRDWMDO 306
 Db 424 PQMNTVELPMGSSSVDVWGNNR--TAADHKYNTSV-LALDATGTGKWKVYNTVHNDLMD- 479
 QY 307 ECTFEMVTVNVDOPTSTEMEGLQSIINPNAATGERVLTGVPCCKTGMQPDATGELF- 364
 Db 480 -----FDLPMQPS-----LVDFPMKDGITKRAVYIGT--KSGQFVLDRYVTKPLTK 524
 QY 365 -----WADTNYQNMIESIDENGIVTNE-----DALIKELD--VEYD 400
 Db 525 VLEODIKVADIPGEQYSTQPSVEMPOIGNOTLKESDMGATPPDQMLCRINFKSMRYD 584
 QY 401 -----VCPPLFGGRDMPASALNDSGIYF-----IPL 427
 Db 585 GLYTPAGTDCVLSIFPGSLGGMWGSIAFDPTHRVFWNDMLGLMLOLIKOTPEDIKQA 644
 QY 428 N---NVCYDMAVAVDOEFTSMQVNTSNTKL--PPGKDMIGRIDAIDISGRTILMSVERA 482
 Db 645 NGGEKVNVTGMGAVPMKGPYKVNKNRPFMSALGIPQOKRPFCTMAIDMKTKQVAMOVPLG 704
 QY 483 AANYT-----PVLTSGGVLFNGCTDRYFRALSOETGELTMOTRL 522
 Db 705 TIQDTPMGINKKLKAPIGMPTIGGPMATOGVLFFATQDYVLRARNSSNGKELMARL 764
 QY 523 ATVASQALISY--EVDGMQVYAIAGGG 547
 Db 765 PYGSGQTPMSTMSRKTQKQYVVSAGG 791

RESULT 14

JC4881
 polyvinyl-alcohol dehydrogenase (acceptor) (EC 1.1.99.23) precursor - Pseudomonas sp.
 N:Alternate names: PVA dehydrogenase
 C:Species: Pseudomonas sp.
 C:Date: 10-Sep-1996 #sequence_revision 18-Oct-1996 #text_change 08-Oct-1999
 R:Shimao, M.; Tamogami, T.; Nishi, K.; Harayama, S.
 C:Accession: JC4881
 J:Shimao, M.; Tamogami, T.; Nishi, K.; Harayama, S.
 A:Title: Cloning and characterization of the gene encoding pyrroloquinoline quinone-d
 A:Reference number: JC4881; MUID:96376165
 A:Accession: JC4881
 A:Molecule type: DNA
 A:Residues: 1-639 <SHI>
 A:Cross-references: DDBJ:D50670; NID:91502278; PIDN:BA09321.1; PID:dl009963; PID:915
 C:Comment: This enzyme is a membrane-bound enzyme. It oxidizes low molecular weight s
 C:Genetics:
 A:Gene: pdh
 C:Keywords: alcohol metabolism; oxidoreductase
 F:1-33/Domain: signal sequence #status predicted <SIG>
 F:49-53/Region: gene C-binding
 F:294-497/Domain: pyrroloquinoline quinone-binding #status predicted <POB>

Query Match 9.0%; Score 276.5; DB 2; Length 639;

Best Local Similarity 22.4%; Pred. No. 2e-11; Matches 143; Conservative 70; Mismatches 241; Indels 183; Gaps 28;

QY 7 LMSAGALLAAPPAPAOQTPVTDLLANPAGEWISYQONENRHSPLDITTEENYQ 66
 DB 117 IWPFPASMPDLPCKKKKIPID--LSTP--DQMGWAGITNAFPOCPCLTADVP 172
 QY 67 LQLMARQMPCKQVQVPLIHGVMYLANPQVIAIDAKTDLTWEHRQPLNATLS 126
 DB 173 LKYMAFN-YPGSKNGQATVVGDRLEFVMSGAVYALNKKTCGYWRHDAANAATSSVAV 231
 QY 127 FGEPTGMAALGTNNYFVSWDNLVALDTATG---QVTFVDYRG-----QGEDM 172
 DB 232 VOLPAGAPAOYA--IFFSDMTKAAVALDAQTKOLMKTITDQPVQMTGSPTEHGLF 289
 QY 173 VNSSGPIYANGVIYVSGCOYSPGCFVSGHDSATGEELMNNYFIP-----RAGEED 226
 DB 290 VPISSG---NEFAINDOMECCKFRGALVALDALSGKVMKTYTQKEPAPFRLNKLK 345
 QY 227 ETWGNDEARMWMTGA--WQIITYDPVTNLV-----HYSTAVGPASETQRTGTP 272
 DB 346 QWNG-----PAGSIMGAPITIDPKRGLVYVATSNSTYEVHSGSDAV----- 387
 QY 273 GGLVYTNRPRAVRPDTGTVIRHQTLPNDNDQCTFEMAVTNVDVOPSTMEGLQSTIN 332
 DB 388 -----NAMEIETGVRMINOVTKDNYLICP---RAANCP-----EKVG 424
 QY 333 PNAATGEREVL-----TGVPCKTGTMOFQDAET--GEFLARDTNYQNMIESIDENG 382
 DB 425 PDFALGNSTPILTLDDGRQYIYVGKSGAVYAMDNDNDGELTMMR----- 469
 QY 383 IYTVNEDALIKELDEYDVCPTFLGRDMPSAALNPDGSIYFIPLNVCYDMMAVDQET 442
 DB 470 -----RVSPGSEL---GGVEF-----GMAADAE-- 489
 QY 443 SMDVY-NTSNVTKLPRGKMIGRIDALIDISTRTLS--VERAANY-----SPVL 490
 DB 490 --NVYVIGISDVITRKGRK--GYVALRIGADYAWAPPAPRTPCRMNNIFCHPAVSQAV 544
 QY 491 STGGVLFNGSTDRYFRALSOETGETLMOTRLA-----TVASGQALSYEVDMQVYATG 545
 DB 545 TAMPGVYFAGSMGDFHRAFTSDGKVLMEFNLAAPRYKTIVAGKQADGGMVQAG-PTTAG 603
 QY 546 GGVSYSGSINALAGERVDSTA-----IGNAVYFAL 577
 DB 604 GMVYVHSG---YAGRSTQNGDLRGREGNVLIAFSV 636

RESULT 15

A1378
 Hypothetical protein (cycB 5' region) - Paracoccus denitrificans (fragment)
 C:Species: Paracoccus denitrificans
 C:Date: 28-May-1992 #sequence_revision 28-May-1992 #text_change 08-Oct-1999
 C:Accession: A1378
 R:Ras, J.; Reijnders, W.N.M.; Van Spanning, R.J.M.; Harms, N.; Oltmann, L.F.; Stouthamer, J. Bacteriol. 173, 6971-6979, 1991
 A:Title: Isolation, sequencing, and mutagenesis of the gene encoding cytochrome c-553i
 A:Reference number: A1378; MUID:92041583
 A:Accession: A1378
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-221 <RAS>
 A:Cross-references: GB:M75583; NID:g150576; PIDN:AAA25574.1; PID:g150577

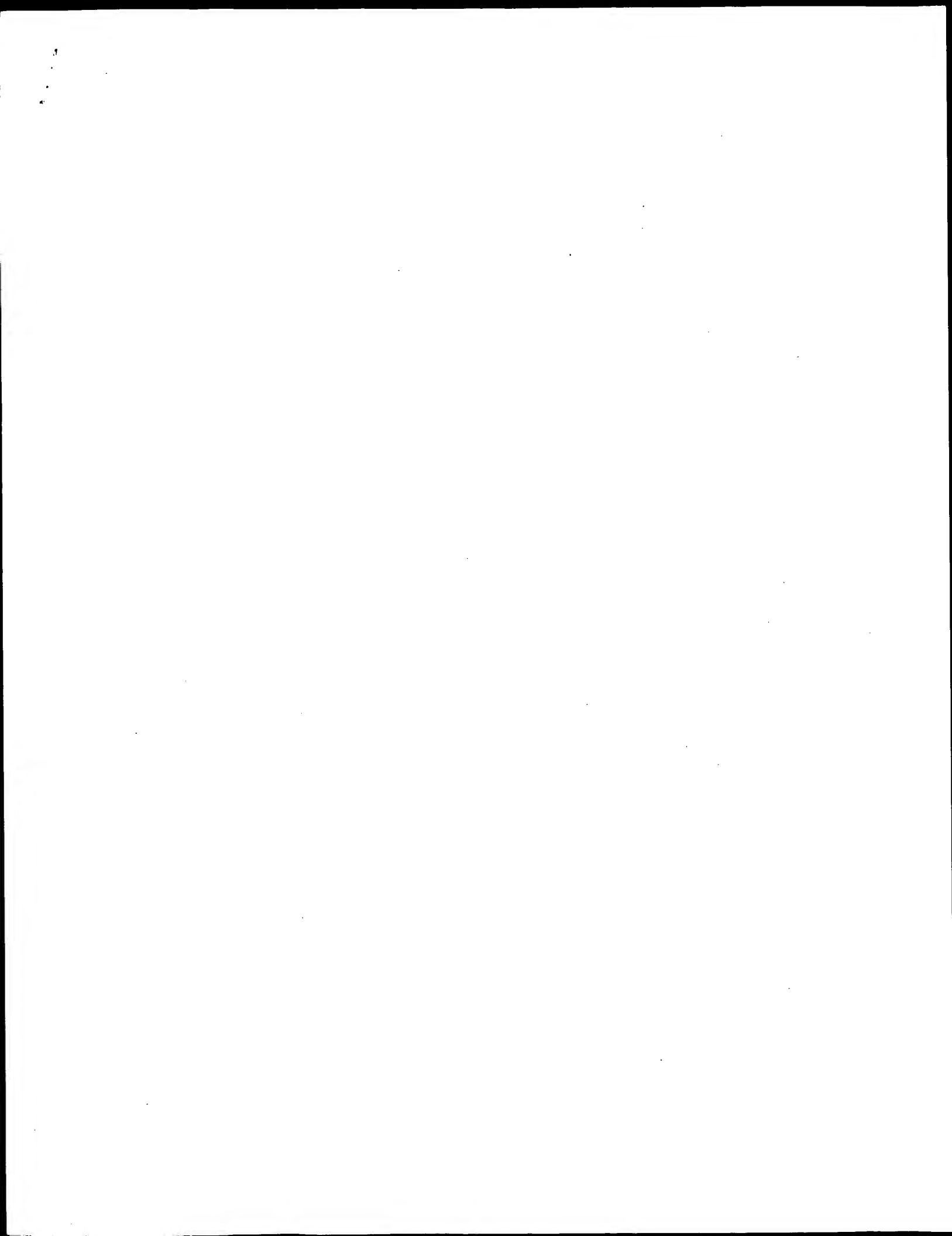
Query Match 7.2%; Score 221.5; DB 2; Length 221;

Best Local Similarity 30.1%; Pred. No. 2.8e-08; Matches 58; Conservative 34; Mismatches 86; Indels 15; Gaps 4;

QY 401 VCPTEFLGDRWPSALNPDGSIYFIPLNVCYDMMAVDQETSMQV--NTSNVTKLPLPG 458
 DB 28 VCPALGTRDQAPAFSPKTNLFYFTNHVCMDEPRVATYTAGOPYGATLSMTAPNS 87

QY 459 KDMIGRIDALIDISTGRTLSVERAANYSPVLSGGVLFNGSTDRYFRALSOETGETLW 518
 DB 88 HGMGNFLAMHNTTGEIKWSVPEQFSVWSGALATAGDVYFYTGLETLKPVDAQTGEELY 147
 QY 519 QTRLATVASGQALSYEVDMQVYATG-----GVSYSGSGLNS-----ALAGERVDS-- 565
 DB 148 KEKTPSGITGNVMTYEHGKQYGVGILSGVGWAGIGLAAGLTNPNDGIGAVGYASLSQY 207
 QY 566 TAIGNAVYFALP 578
 DB 208 TELGGQLTFEELP 220

Search completed: August 8, 2001, 19:40:33
 Job time: 30 sec



Matches 165; Conservative 85; Mismatches 268; Indels 66; Gaps 14;

OY 10 SAGALALLAARFAQVTVPTD-----LLANPAGEWISYGOENRHSPLTQIT 61
 DB 17 TAGTICALISGYATMASADGQATGEALIHADHPNMWMTYRTYSEORYSPLDQINR 76
 OY 62 ENVGOLQIWMANGMOPKQVQV-TPLIHGVMYLANPGVIOAIIDAKTGLIWEHRRLP 119
 DB 77 SNVGLKIAMLYLDLTNRGQEGTPLYIDGVYATTNMSMKAVAAATGKILMSYDPRPG 136
 OY 120 NIATLNSFGEPTRGMAIXGTNYEVSMDNHLVADTATGVTDPVDRGQEDVNSN- 175
 DB 137 NIADKGCDDTVNRGAAYWNGKVFETGEGRLIALDAKTGLWMSVNTLPPAEELGKGRSY 196
 OY 176 --SSGPIVANGVIAGSVCQSPFGC--FVSGHSATGEELMRNYETPRAGEEDTWCN 231
 DB 197 TVDGAFLAKRVIIGN--GGSEFGARGFVAFETGKVDMPREFTPAPNKPNEPDHNASD 254
 OY 232 D-----YEARMMTGA-----WGOLTYDPVTNLVHGSTAVGPASETORGTGCT 275
 DB 255 SVLMKKAQVQWSPGTGAMTRGQGGTVMDSIYDPVADLVILGVNGSPWNYKYSSEKGD 314
 OY 276 LYGNTRPRAVAPDTEIYVNRHQLPRDNMDQECTFEKMAVTVNDVQSTEMEGLOSINPNA 335
 DB 315 NLFLGSIYALKPTEGYEYVNHQETPMQMDFTSVQOITMLDLPINGET----- 362
 OY 336 ATGERRVLTGVPCKGTGTMQPDATGEFLMARDNVYONMIESID-ENGITVWEDATLKE 394
 DB 363 -----RHVIYVAP-KNGFFIIDAKTGEISGKIVYVMAASGDPKGRPIYNDALYTL 417
 OY 395 LDVEYDVCPTFLGGRDPSAALNPDGSIYFIPLNNVCYDMAVADQET--SMDVYNTS--- 450
 DB 418 TGRMYGCIPLGDLGSHNFAAFSPKGTGLVYIPAOQVPELTNGVGTTPRPSDMNLGLDM 477
 OY 451 NVTKLPPG-----KDMIGRIDALISTGRTILMSYERAAVNSPYLSTGGCVLENGGT 502
 DB 478 NKVGIPSPSEAKQAFVVDLKGWIVAMPDQKQAEAMRVDRHKGPNWNGILLATGDLLEQGLA 537
 OY 503 DRYFRALSOETGETIMOTRLATVASSGQAISEYDGMQVYAIAGG 546
 DB 538 NGEPHAYDATNGSDLFHFAADSGIAPVYTLANGKOYVAVEVG 581

RESULT 2
 DHET_ACEPO STANDARD; PRT; 738 AA.
 AC P28036;
 DT 01-AUG-1992 (Rel. 23, Created)
 DT 01-AUG-1992 (Rel. 23, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE ALCOHOL DEHYDROGENASE [ACCEPTOR] PRECURSOR (EC 1.1.99.8).
 GN ADHA.
 OS Acetobacter polyoxogenes.
 OC Bacteria; Proteobacteria; alpha subdivision; Acetobacteraceae;
 OC Acetobacter.
 OX NCBI_TaxID=439;
 RN [1]
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RC STRAIN-NB11028;
 RC MEDLINE=91159482; PubMed=2001402;
 RA Tamaki T., Fukaya M., Takemura H., Tayama K., Okumura H.,
 RA Kawamura Y., Nishiyama M., Horinouchi S., Beppu T.;
 RT Cloning and sequencing of the gene cluster encoding two subunits of
 RT membrane-bound alcohol dehydrogenase from Acetobacter polyoxogenes.";
 RL Biochim. Biophys. Acta 1088:292-300(1991).
 CC -1- FUNCTION: DEHYDRATION OF PRIMARY ALCOHOLS (EXCEPTION: METHANOL).
 CC -1- CATALYTIC ACTIVITY: PRIMARY ALCOHOL + ACCEPTOR = ALDEHYDE +
 CC REDUCED ACCEPTOR.
 CC -1- COFACTOR: POQ AND HEME.
 CC -1- SUBUNIT: HETEROTETRAMER (DEHYDROGENASE, CYTOCHROME, AND TWO
 CC SMALLER UNKNOWN SUBUNITS) THAT FORMS THE ALCOHOL DEHYDROGENASE
 CC COMPLEX.
 CC -1- SUBCELLULAR LOCATION: MEMBRANE-BOUND, FACING THE PERIPLASMIC

CC SPACE (POTENTIAL).
 CC -1- SIMILARITY: BELONGS TO THE BACTERIAL POQ DEHYDROGENASE FAMILY.
 CC CC
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 CC CC
 CC EMBL: D00635; BAA00528.1; -
 CC PIR: S14270; S14270.
 CC DR HSSP: P22619; 2MTA.
 CC DR InterPro: IPR000345; -
 CC DR InterPro: IPR001479; -
 CC DR InterPro: IPR002372; -
 CC DR Pfam: PF01011; Bacterial_POQ_6.
 CC DR PROSITE: PS00363; BACTERIAL_POQ_1; 1.
 CC DR PROSITE: PS00364; BACTERIAL_POQ_2; 1.
 CC DR PROSITE: PS00190; CYTOCHROME_C; 1.
 CC DR OXidoreductase; POQ; Heme; Periplasmic; Membrane; Signal.
 CC KW SIGNAL 1 35
 CC FT CHAIN 36 738 ALCOHOL DEHYDROGENASE [ACCEPTOR].
 CC FT BINDING 650 650 HEME (COVALENT) (BY SIMILARITY).
 CC FT BINDING 653 653 HEME (COVALENT) (BY SIMILARITY).
 CC FT METAL 654 654 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
 CC SQ SEQUENCE 738 AA; 80840 MW; 1E2B6ED7BCD92AF6 CRC64;
 CC
 CC Query Match 18.3%; Score 564.5; DB 1; Length 738;
 CC Best Local Similarity 28.0%; Pred. No. 5.7e-32;
 CC Matches 165; Conservative 85; Mismatches 261; Indels 79; Gaps 14;

OY 10 SAGALALLAARFAQVTVPTD-----LLANPAGEWISYGOENRHSPLTQIT 61
 DB 17 TAGTICALISGYATMASADGQATGEALIHADHPNMWMTYRTYSEORYSPLDQINR 76
 OY 62 ENVGOLQIWMANGMOPKQVQV-TPLIHGVMYLANPGVIOAIIDAKTGLIWEHRRLP 119
 DB 77 SNVGLKIAMLYLDLTNRGQEGTPLYIDGVYATTNMSMKAVAAATGKILMSYDPRPG 136
 OY 120 NIATLNSFGEPTRGMAIXGTNYEVSMDNHLVADTATGVTDPVDRGQEDVNSN- 175
 DB 137 NIADKGCDDTVNRGAAYWNGKVFETGEGRLIALDAKTGLWMSVNTLPPAEELGKGRSY 196
 OY 176 --SSGPIVANGVIAGSVCQSPFGC--FVSGHSATGEELMRNYETPRAGEEDTWCN 231
 DB 197 TVDGAFLAKRVIIGN--GGSEFGARGFVAFETGKVDMPREFTPAPNKPNEPDHNASD 254
 OY 232 D-----YEARMMTGA-----WGOLTYDPVTNLVHGSTAVGPASETORGTGCT 275
 DB 255 SVLMKKAQVQWSPGTGAMTRGQGGTVMDSIYDPVADLVILGVNGSPWNYKYSSEKGD 314
 OY 276 LYGNTRPRAVAPDTEIYVNRHQLPRDNMDQECTFEKMAVTVNDVQSTEMEGLOSINPNA 335
 DB 315 NLFLGSIYALKPTEGYEYVNHQETPMQMDFTSVQOITMLDLPINGET----- 362
 OY 336 ATGERRVLTGVPCKGTGTMQPDATGEFLMARDNVYONMIESID-ENGITVWEDATLKE 394
 DB 363 -----RHVIYVAP-KNGFFIIDAKTGEISGKIVYVMAASGDPKGRPIYNDALYTL 417
 OY 395 LDVEYDVCPTFLGGRDPSAALNPDGSIYFIPLNNVCYDMAVADQET--SMDVYNTS--- 450
 DB 418 TGRMYGCIPLGDLGSHNFAAFSPKGTGLVYIPAOQVPELTNGVGTTPRPSDMNLGLDM 477
 OY 451 NVTKLPPG-----KDMIGRIDALISTGRTILMSYERAAVNSPYLSTGGCVLENGGT 502
 DB 478 NKVGIPSPSEAKQAFVVDLKGWIVAMPDQKQAEAMRVDRHKGPNWNGILLATGDLLEQGLA 537
 OY 503 DRYFRALSOETGETIMOTRLATVASSGQAISEYDGMQVYAIAGG 546
 DB 538 NGEPHAYDATNGSDLFHFAADSGIAPVYTLANGKOYVAVEVG 581

OY 270 GTPGGLTGTMTREAVRPDTEIYVNRHQLPRDNMDQECTFEKMAVTVNDVQSTEMEGLO 329
 DB 308 SEGKGDNLFLGSIYALKPTEGYEYVNHQETPMQMDFTSDQITMLDLP----- 357
 OY 330 SINPNAATGERRVLTGVPCKGTGTMQPDATGEFLMARDNVYONMIESID-ENGITVNE 388
 DB 358 -----NGEYRHVIVHARKNGFEYIIDAKTGEISGKIVYVMAASGDLPKTRPIYNP 410
 OY 369 DALIKELDEVDVCTFLGGRDMSAALNPDGSIYFIPLNNVCYDMAVADQET--SMDVY 447
 DB 411 DALYTLNGKEWYGIPLDGLGSHNFAAFSPKGTGLVYIPAOQVPELTNGVGTTPRPSDSW 470
 OY 448 NTS--NVTKLPPG-----KDMIGRIDALISTGRTILMSYERAAVNSPYLSTGGV 496
 DB 471 NLGIDMKNVGIPLDSEPKQAFVVDLKGWIVAMPDQKQAEAMRVDRHKGPNWNGILLATGDL 530
 OY 497 LFGGTDRYFRALSOETGETIMOTRLATVASSGQAISEYDGMQVYAIAGG 546
 DB 531 LFOGLANGFEHAYDATNGSDLFHFAADSGIAPVYTLANGKOYVAVEVG 580

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RESULT 3
DHET_GLUSU STANDARD; PRT; 757 AA.
AC 005542;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE ALCOHOL DEHYDROGENASE [ACCEPTOR] PRECURSOR (EC 1.1.99.8) (G3-ADH
DE SUBUNIT 1).
GN ADHA.
OS Gluconobacter suboxydans.
OC Bacteria; Proteobacteria; alpha subdivision; Acetobacteraceae;
OC Gluconobacter.
OC NCBI_TaxID=443;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 36-50.
RC STRAIN=IPO.12528;
RX MEDLINE=97208225; PubMed=9055427;
RA Kondo K., Horinouchi S.;
RT "Characterization of the genes encoding the three-component membrane-
RT bound alcohol dehydrogenase from Gluconobacter suboxydans and their
RT expression in Acetobacter pasteurianus."
RT Appl. Environ. Microbiol. 63:1131-1138(1997).
CC -1- FUNCTION: DEHYDRATION OF PRIMARY ALCOHOLS (EXCEPTION: METHANOL)
CC -1- (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: PRIMARY ALCOHOL + ACCEPTOR = ALDEHYDE +
CC -1- REDUCED ACCEPTOR.
CC -1- COFACTOR: POQ AND HEME.
CC -1- SUBUNIT: HETEROTRIMER (DEHYDROGENASE, CYTOCHROME AND PROTEIN
CC ADHS), THAT FORMS THE ALCOHOL DEHYDROGENASE COMPLEX.
CC -1- SUBCELLULAR LOCATION: MEMBRANE-BOUND, FACING THE PERIPLASMIC
CC SPACE (POTENTIAL).
CC -1- SIMILARITY: BELONGS TO THE BACTERIAL POQ DEHYDROGENASE FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; D86375; BAA19753.1; -.
DR HSSP; P38339; 4AAH.
DR InterPro; IPR000345; -.
DR InterPro; IPR001479; -.
DR InterPro; IPR002372; -.
DR Pfam; PF01011; Bacterial_POQ_6.
DR PROSITE; PS00363; BACTERIAL_POQ_1; 1.
DR PROSITE; PS00364; BACTERIAL_POQ_2; 1.
DR PROSITE; PS00190; CYTOCHROME_C; 1.
KW Oxidoreductase; POQ; Heme; Periplasmic; Membrane; Signal.
FT SIGNAL 1 34
FT CHAIN 35 757 ALCOHOL DEHYDROGENASE [ACCEPTOR].
FT MOD_RES 35 35 PYROLIDONE CARBOXYLIC ACID.
FT ACT_SITE 342 342 BASE (POTENTIAL).
FT BINDING 653 653 HEME (COVALENT) (BY SIMILARITY).
FT BINDING 656 656 HEME (COVALENT) (BY SIMILARITY).
FT METAL 657 657 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
SQ SEQUENCE 757 AA; 82968 MW; 39B9F90E3B947581 CRC64;

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Query Match 17.9%; Score 553.5; DB 1; Length 757;
Best Local Similarity 27.4%; Pred. No. 3.5e-31;
Matches 168; Conservative 97; Mismatches 253; Indels 93; Gaps 19;

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QY 7 LWASGATALLAA--PAAQV---TPVTDLLANPAGEWISYGCNQNRHSPLTQITTT 61
DB 16 LLSCAALAFSAAYVAFAQEDTGAITSNDGHP-CDWLSYSGRSYEGRSPLDQINT 74
QY 62 ENVGOLQLVWANGMQPKVQV-TPLIHGVMTLANPGVDTAIDAKTDLLIWEHRQLP- 119

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DB 75 ENVGKILAMHEDLTNRGOECTPLIVGVYATTNWMSKMAALDAATGKLMSYDPKVG 134
QY 120 NATIATNSGEPTRGALXGNTNYEYSMDNLVADDTAGOVTFVDROGQEDVSN---- 175
DB 135 NIADRGCCDVSRAAYNKGAVYFGTFDGRLLIADAKTKGLWSTYTTTPKNOLOHOSY 194
QY 176 --SSGPIVANGVIVASTCOYSPFGC--FVSGHDSATGEELMRNYFIPRAGEBD---- 226
DB 195 TYDGAAPRIAKGKVLIGN--GGAEEFARGFVSAPDAETSKLDMRFTVNPENKPDGAASD 252
QY 227 -----ETWGNDYEARMTG---AMQITDPTNLVHSGTAVGPASETGRTPGGT 275
DB 253 DILMSKAYPTWGNKAMKQGGGTWDSLVYDPTDLVYLGVGSGSPWNTKFNSEKGD 312
QY 276 LYGNTFRFAVRPDGTGEIYVRHOTLPRDMMDOCTPEMMYTNVDVQPTMEGLSINPA 335
DB 313 NLFSGIYAINPDYTKYVWHFQETPMDEMDYTSVOQIMTLDMPV----- 356
QY 336 ANGE--RRVLTGVPCRTGTMMQFPAETGEFLMARDTNYONMIESIDE-NGITYNEDAILK 393
DB 357 -NGEMRHVIVHAP-KNGFYIIDAKTGKFTGKPYTEENWANGLDPVIGRPYVPDALMT 414
QY 394 ELDEYDVCPPTLGGHWPSSALNPDGSGITFPLNNV-----CYDMAAYDQE 440
DB 415 LYGKPPWLGIPGELGHNFAAMAYSPKTKLYIPAOQIPLLYDGKGRKAYHDANNLGLD 474
QY 441 FTSMDVYNTSNVTKLPPGDMIGRIDADISTGRTL-NSVERAANYS-----PVL 490
DB 475 MNKIGLFDNDPEHVAAKDF-----LKVLGWIVAMPPEKMAAFITNHGPNNGLL 528
QY 491 STGGGVLFNGGDRYFRALSOETGETLMOTRLATVYASGAISIEVDGMOYAI----- 543
DB 529 ATAGNVIFQGLANGEFHAYDATNGNDLYSFPASALIAAPPVYTAGKQYVAVEVGQI 588
QY 544 ---AGGVSYSGS 553
DB 589 YPFLYGVGVAARTSG 601

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RESULT 4
DHET_ACCEAC STANDARD; PRT; 742 AA.
AC P18278;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE ALCOHOL DEHYDROGENASE [ACCEPTOR] PRECURSOR (EC 1.1.99.8).
GN ADHA OR ADHI.
OS Acetobacter aceti.
OC Bacteria; Proteobacteria; alpha subdivision; Acetobacteraceae;
OC Acetobacter.
OC NCBI_TaxID=435;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 36-50.
RX MEDLINE=89255070; PubMed=2722742;
RA Inoue T., Sunagawa M., Mori A., Imai C., Fukuda M., Takagi M.,
RA Yano K.;
RT "Cloning and sequencing of the gene encoding the 72-kilodalton
RT dehydrogenase subunit of alcohol dehydrogenase from Acetobacter
RT aceti."
RT J. Bacteriol. 171:3115-3122(1989).
RN [2]
RP 3D-STRUCTURE MODELING.
RX MEDLINE=95289964; PubMed=7772016;
RA Gozier G.E., Gilles I.G., Anthony C.;
RT "The structure of the quinoprotein alcohol dehydrogenase of
RT Acetobacter aceti modelled on that of methanol dehydrogenase from
RT Methylobacterium extorquens."
RT Biochem. J. 308:375-379(1995).
CC -1- CATALYTIC ACTIVITY: PRIMARY ALCOHOL + ACCEPTOR = ALDEHYDE +
CC -1- REDUCED ACCEPTOR.
CC -1- COFACTOR: POQ AND HEME.

```

CC -1- SUBUNIT: TETRAMER OF NON IDENTICAL CHAINS (DEHYDROGENASE,
CYTOCHROME, AND TWO SMALLER UNKNOWN SUBUNITS).
CC -1- SUBCELLULAR LOCATION: PERIPLASMIC.
CC -1- SIMILARITY: BELONGS TO THE BACTERIAL PQQ DEHYDROGENASE FAMILY.
CC -----
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CC -----
DR EMBL; D90004; BAAL4058.1; -
DR PIR; J50326; J50326.
DR HSSP; P38539; 4AAH.
DR InterPro; IPR000345; -
DR InterPro; IPR001475; -
DR InterPro; IPR002372; -
DR Pfam; PF01011; Bacterial_PQQ; 6.
DR PROSITE; PS00363; BACTERIAL_PQQ_1; 1.
DR PROSITE; PS00364; BACTERIAL_PQQ_2; 1.
DR PROSITE; PS00190; CYTOCHROME_C; 1.
KW Oxidoreductase; PQQ; Heme; Periplasmic; Membrane; signal.
FT SIGNAL 1 35
FT CHAIN 36 742
FT ACT_SITE 343 343 BASE (POTENTIAL).
FT BINDING 649 649 HEME (COVALENT) (BY SIMILARITY).
FT BINDING 652 652 HEME (COVALENT) (BY SIMILARITY).
FT METAL 653 653 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
SQ SEQUENCE 742 AA; 81521 MW; 9C6C9268DB825A CRC64;

Query Match 17.7%; Score 547.5; DB 1; Length 742;
Best Local Similarity 27.8%; Pred. No. 8.8e-31;
Matches 176; Conservative 97; Mismatches 244; Indels 115; Gaps 24;

11 AGALALLAAPAAVPTVDEL--ANPPAGEWISYQONENRHSPLITITENVGOLD 68
23 AALPYAAVPARADQGTGEALIHADHPENMLSYGRYSSEGRYSPLDINSNVGDLK 82
69 LVMARGQOPKQV-VTPPLINDGWYTLNPGDVLQADAKTGDLIWEHRQLP-NIATLNS 126
83 LLAGYTLDTNNGQATPLVVDGIMYATNTNMSKKEALDAAATGKLLMOYDPKVINADKGC 142
127 FGEPTRGALYGTNVYFVSWDNHLVALDPTATGOV-----TEVDROGGEGEMVSNSSGPI- 180
143 CDYVNRAGYVNGVYFMTGTDGRILVADADATGKKVAVNTIPADASLGKORSTYVDGAVR 202
181 VANGVIVAGSTCOYSPFGC--FVSGHDSATGEELMRNYFLPRAEGEGD----- 226
203 VANGVIVAGSTCOYSPFGC--FVSGHDSATGEELMRNYFLPRAEGEGD----- 226
227 -ETMNGNDYEAARMT-----GAMQIYDPTNLYVHGSYAVGASSETORGTGGTLY--- 277
261 YKTMGP--KAMVYRGGGGGTWDSLVYDVSLLY---LAVG-----NGSPNNYRSE 309
278 -GTN-----TRFAVRPDTGEIVRHOITLPPDNNDQCTEFEMVNTVNDVOPSTMEGLQSI 331
310 GIGSNFLFISIVALKPTEGYVNHPRATPDMDQDYSVQGIATLIDMPK----- 358
332 NPNAATGE--RVLTGVPCATGTMMQDAETGEFLMARDNTYONMIESID-----EN 381
359 -----GEMHNVIVAP--KNGFEYVLDATKGEFLSGKNVYVQWANGDLPLVGRPMYND 411
382 GIYTVNEDALIKELDYEVDCYPLFLGGRMPSSAALNPDGSIYFIPLNNCY----- 432
412 GIYTVNEDALIKELDYEVDCYPLFLGGRMPSSAALNPDGSIYFIPLNNCY----- 432
433 -----DMVAVDQFTSMDEVNTSNVTKLPPGKDMIGRIDIDISTGRTILMSYRAAANSP 488
464 KPHADSNNVGLDMTKGLPDITE--ARTATIKDLHGMLLAMDVPMKMETYWKIDHKPFWNG 522

QY 489 VLSNGGVLENGGDRFRALSGETGELMOTPLATVAGQAISYEVDMQVYA----- 542
DB 523 ILATGGDLFLQGLANDEFHAYDATNGSDLYKFDQAQGIATPMTYSVNGQYAAVEVGNG 582
QY 543 -----IAGGVSYSGSL-----NSALAGERVDSTA 567
DB 583 GIYPLSMGVGYSRGSMTVNHSTYIAAFSLDCKA 614
RESULT 5
ID EXAA_PSEAE STANDARD; PRT; 623 AA.
AC 092417;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE QUINOPROTEIN ETHANOL DEHYDROGENASE PRECURSOR (CC 1.1.99.-) (OEHD).
GN EXAA OR PA1982.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 17933;
RX MEDLINE=99041560; PubMed=9826187;
RA Diehl A., Wintzingerode F., Goerlich H.;
RT "Quinoprotein ethanol dehydrogenase of Pseudomonas aeruginosa is a
RT homodimer: sequence of the gene and deduced structural properties of
RT the enzyme.";
RL Eur. J. Biochem. 257:409-419(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=PA01;
RX MEDLINE=20437337; PubMed=10984043;
RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrenner P.,
RA Hickey M.J., Brinkman F.S.L., Huftagle W.O., Kowalik D.J., Lagrou M.,
RA Garber R.L., Goltzy L., Tolentino E., Westbrook-Wadman S., Yuan Y.,
RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Laidig K., Lim R.M.,
RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
RA Reiter J., Salter M.H., Hancock R.E.W., Lory S., Olson M.V.;
RT "Complete genome sequence of Pseudomonas aeruginosa PA01, an
RT opportunistic pathogen.";
RL Nature 406:959-964(2000).
RN [3]
RP SEQUENCE OF 1-52 FROM N.A.
RC STRAIN=ATCC 17933;
RX MEDLINE=99173751; PubMed=10075429;
RA Schober M., Goerlich H.;
RT "Cytochrome c550 is an essential component of the quinoprotein ethanol
RT oxidation system in Pseudomonas aeruginosa: cloning and sequencing of
RT the genes encoding cytochrome c550 and an adjacent acetaldehyde
RT dehydrogenase.";
RL Microbiology 145:471-481(1999).
RN [4]
RP X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS) OF 35-616.
RC STRAIN=ATCC 17933;
RX MEDLINE=20202376; PubMed=10736230;
RA Ketel T., Diehl A., Knaute T., Stezowski J.J., Hoehne W.,
RA Goerlich H.;
RT "X-ray structure of the quinoprotein ethanol dehydrogenase from
RT Pseudomonas aeruginosa: basis of substrate specificity.";
RL J. Mol. Biol. 297:961-974(2000).
CC -1- FUNCTION: OXIDIZE PRIMARY ALCOHOLS AND ALSO ACTS ON SECONDARY
CC ALCOHOL, BUT NOT HIGHLY ACTIVE ON METHANOL.
CC -1- COFACTOR: PQQ AND CALCIUM.
CC -1- SUBUNIT: HOMODIMER.
CC -1- SUBCELLULAR LOCATION: PERIPLASMIC.
CC -1- SIMILARITY: BELONGS TO THE BACTERIAL PQQ DEHYDROGENASE FAMILY.
CC -----
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DR EMBL: AJ009858; CA00896.1; -
DR EMBL: AE004624; AAC05370.1; -
DR EMBL: AF068264; AAC79657.1; -
DR PDB: 1PLG; 30-AUG-00.
DR InterPro: IPR002372; -
DR Pfam: PF01011; Bacterial_P00_1; FALSE_NEG.
DR PROSITE: PS00363; BACTERIAL_P00_1; FALSE_NEG.
DR PROSITE: PS00364; BACTERIAL_P00_2; FALSE_NEG.
KW Oxidoreductase; PQQ; Periplasmic; Signal; Calcium; 3D-structure.
FT SIGNAL 1 34
FT CHAIN 1 35 623 QUINOPROTEIN ETHANOL DEHYDROGENASE.
FT DISULFID 139 140
SQ SEQUENCE 623 AA; 68123 MW; 32DDE5DF20B291D6 CRC64;

Query Match 16.3%; Score 505; DB 1; Length 623;
Best Local Similarity 25.7%; Pred. No. 6.5e-28;
Matches 164; Conservative 105; Mismatches 276; Indels 92; Gaps 23;

3 PSLMASGALAL--LAAPFAQVTPVDEL--PPAGEWISYQONENRHSPLT 57
1 PSLMASGALAL--LAAPFAQVTPVDEL--PPAGEWISYQONENRHSPLT 57
9 PAGLRLPSLHCLAFVALGASGALAKDVTWEDIANDKTTDVLQYGGTGAQWSPK 68
58 QTTENVGOLQVWARGM--QPGKVOYTPLIHGWMLANPGDYLQATDAKTDLWE 113
1 QTTENVGOLQVWARGM--QPGKVOYTPLIHGWMLANPGDYLQATDAKTDLWE 113
69 QVANADVFLTPAWSYSEFGEKORQ--ESQALVSDGVIVTYSRFLPAKTKRLMT 127
114 HRRQLEN--IATNNGEPTRGALVTNVPFVSMNHLVALDPTAGVTFD--VD 165
128 YHRLPDLRPPCDVYN--RGAITGDKVFFGTDLASVALNKNTGKWKKKRAD 181
166 RQGEDMVSNSGPIVANG--VIVAGSTQYSPFGE--VSGHDSATGEELMRNFTI 218
182 HGAGYTM--TGAPTYKDKGTGKVLIIHSS--GDEFVGRFLRFPDPTGGEIMRPFV 237
219 PR-----AGEBDETWGNDYEA--RWMGCA--WGQIYDVTNLVNHG 257
238 EGHMRLNGKSTVTGDKVAPSPWDDRNSPTGKVESWSHGGAPWQASAFDAETVILV 297
258 STAVGASEFQRTGPG-----TLGTNTREAVRPTGEIWRHRTLPDRNMDQECTFE 311
298 AGNPGWNTWARTAKGNGHDSLT--TSGOYGVDPSSSEVKNFIOHTPDNDAMSSGNNE 356
312 MMTNVQVPTSTEMEGLQSIINP--AATGERVLTGPKCTGTW--QFDAETGEFL 364
357 LVLEFDYKAKDKIVKATTAHADRNCFYVDRSGKQLQNAFPPVDNITWASHIDLTG-- 413
365 WADDTYQNMIESIDNGIYTVNEDAILKELDEYVOCFTFLGRMPASALNPPSGIYF 424
414 --RPVEREQRPLPBPQ-----QKHGKAVESPPFLGGKWNPMAYSDQDGLFY 461
425 IPIANNVCYDMAVDOEFTSDVYNTSNVTKLPKGMKIDRIDALIDSTGRITSEVERAA 484
462 VPANHHKEDYWTPEVSYTGSALGKGFIRKRYDDHVSGLRAMPVDSKRYVWEHNEHLP 521
485 NYSPLVSTGGVLENGSTDRFERRALSQETGELIMQRLTAVASGQALSYEDMOYVATA 544
522 LMGVGLATAGNLVFTGTGDFYKAFDAKSGKELMKPOTSGSIVSPITWEDGEOYLGYT 581
545 GGVSVSGSLNSALAGERDST--ALGNNAVYFALP 578
582 ---VGYG-GAVPLMGDMADLTRPVAQSGSFWFKLP 614

RESULT 6
DHML_PARDE STANDARD; PRT; 631 AA.
ID DHML_PARDE
AC P1293;

DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE METHANOL DEHYDROGENASE SUBUNIT 1 PRECURSOR (EC 1.1.99.8) (MDH LARGE
DE ALPHA SUBUNIT) (MEDH).
GN MOXF.
OS Paracoccus denitrificans.
OC Bacteria; Proteobacteria; alpha subdivision; Rhodobacter group;
OC Paracoccus.
OX NCBI_TaxID=266;
RN [1]
RP SEQUENCE FROM N.A. AND SEQUENCE OF 33-49.
RX MEDLINE=87307969; PubMed=3114231.
RA Harms N., de Vries G.E., Maurer K., Hoogenkamp J., Stouthamer A.H.;
RT "Isolation and nucleotide sequence of the methanol dehydrogenase
RT structural gene from Paracoccus denitrificans."
RL J. Bacteriol. 169:3969-3975(1987).
CC -1- CATALYTIC ACTIVITY: PRIMARY ALCOHOL + ACCEPTOR - ALDEHYDE +
CC REDUCED ACCEPTOR.
CC -1- COFACTOR: PQQ.
CC -1- SUBCELLULAR LOCATION: PERIPLASMIC.
CC -1- MISCELLANEOUS: MDH IS THE MAJOR PROTEIN IN THE CELL DURING GROWTH
CC ON METHANOL. (IN P. DENITRIFICANS MDH CONSTITUTES UP TO 15% OF THE
CC TOTAL CELL PROTEIN).
CC -1- SIMILARITY: BELONGS TO THE BACTERIAL PQQ DEHYDROGENASE FAMILY.
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch)
CC EMBL: M17339; AAAH
DR HSP: P38539; AAAH
DR InterPro: IPR001479; -
DR InterPro: IPR002372; -
DR Pfam: PF01011; Bacterial_P00_1; 7.
DR PROSITE: PS00363; BACTERIAL_P00_1; 1.
DR PROSITE: PS00364; BACTERIAL_P00_2; 1.
KW Oxidoreductase; PQQ; Signal; Methanol utilization; Periplasmic.
FT SIGNAL 1 32
FT CHAIN 1 33 631 METHANOL DEHYDROGENASE SUBUNIT 1.
FT DISULFID 135 136 BY SIMILARITY.
FT DISULFID 418 447 BY SIMILARITY.
FT ACT SITE 335 335 BASE (POTENTIAL).
SQ SEQUENCE 631 AA; 69799 MW; 0934DC93PFC5730B CRC64;

Query Match 16.0%; Score 495; DB 1; Length 631;
Best Local Similarity 26.0%; Pred. No. 3.3e-27;
Matches 166; Conservative 111; Mismatches 259; Indels 102; Gaps 25;

4 TSLMASGALAL--LAAPFAQVTPVDEL--LANPAGWISYQONENRHSPLT 60
1 TSLMASGALAL--LAAPFAQVTPVDEL--LANPAGWISYQONENRHSPLT 60
12 SLSAAVAVMGALVITTAATA--NDQVLELAKDP--NMWGRGDRNAQYSEMDIN 65
61 TENVGOLQV--ARGMPGKVQVTPLIHDCVMIYLANP--GDVQIADA--KTGDLIWEHR- 115
66 KENVQQLRANFSFGVLHGH--EGTFPLVGDGRMTIHFPPTTALDNEGKILMOKRP 124
116 RQPLNATLNSGEPTRGMALYGTN-----VYFVSWNHLVALDPTAGVTFVDYDQOG 169
125 KNPARTVACCDVNNRSLAYWPGDDQKPLFRTQDGHIVAMDQETGRWIMENSIDI 184
170 EDMVNSGPIVANGVYAGSTQYSPFGEVSGHDSATGEELMRNFTI----- 218
185 KVGSTLTITAPYIKDLVIVGSSGAEIVRGVYTAIVKSGEMRRARFTGDEDELLAED 244
219 -----PRAGEE--GDETWGNDYEARMGTGA--WGQIYDVTNLVNHGSTAVGASETO 268
245 FNAPRPHYGKAKNLGLETWEGD--AMKIGGGINMGWYVYDEVDLEFYGSGNPPAMNETM 301

RT Methylobacterium organophilum XX methanol dehydrogenase structural
 RT gene." ;
 RL J. Bacteriol. 170:4739-4747(1988).
 CC -1- CATALYTIC ACTIVITY: PRIMARY ALCOHOL + ACCEPTOR = ALDEHYDE +
 CC REDUCED ACCEPTOR.
 CC -1- COFACTOR: POO.
 CC -1- SUBUNIT: THE HOLOENZYME MDH HAS AN ALPHA-2/BETA-2 CONFIGURATION
 CC OF A LARGE ALPHA AND A SMALL BETA SUBUNIT.
 CC -1- SUBCELLULAR LOCATION: PERIPLASMIC, BUT ASSOCIATED WITH INNER
 CC MEMBRANE.
 CC -1- SIMILARITY: BELONGS TO THE BACTERIAL POO DEHYDROGENASE FAMILY.
 CC
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 CC
 CC EMBL: M22629; AAA50289.1; -
 CC HSSP: P38539; 4AAH.
 CC InterPro: IPR001479; -
 CC InterPro: IPR002372; -
 CC Pfam: PF01011; Bacterial_POO.7.
 CC DR PROSITE: PS00363; BACTERIAL_POO.1; 1.
 CC DR PROSITE: PS00364; BACTERIAL_POO.2; 1.
 CC KW Oxidoreductase; POO; Signal; Methanol utilization; Periplasmic.
 CC FT SIGNAL 28
 CC FT CHAIN 29 626 METHANOL DEHYDROGENASE SUBUNIT 1.
 CC FT DISULFID 130 131 BY SIMILARITY.
 CC FT DISULFID 413 442 BY SIMILARITY.
 CC FT ACT_SITE 330 330 BASE (POTENTIAL).
 CC FT SEQUENCE 626 AA; 68677 MW; 8768F6B8371E5DF CRC64;

Query Match 15.5%; Score 477.5; DB 1; Length 626;
 Best Local Similarity 26.0%; Pred. No. 5.4e-26;
 Matches 163; Conservative 112; Mismatches 267; Indels 85; Gaps 25;

QY 10 SAGALALLA-AP-AFAQVPTVDELAPPAGE-WISYQNGENRHSPLTQTTERVQ 66
 DB 7 SVSALAMALAPALSSVAAVANDKVELSKSDNMWMPGRNYSNNSELKQVKNKSVKQ 66
 QY 67 LQIYW-ARGQOPKQVQVPLIHGVWL--ANPGVIOAIDA-KTGDILWEHR-ROLPN 120
 DB 67 LRPAMTSTGLLNCH-EGAPLVVDGAMVHTSPNNTF-ALDLDDPGHIIKODKPNQPA 124
 QY 121 IATNSFGEPRGMALYGTN-----VYFVSWNHLVALDTATGQVTFDVRGOGEDMVS 174
 DB 125 ARAYACCDIVARGLAYWPGSGKTPALLIKTQLDHRVVALNAETGEIVKVENSDIKVST 184
 QY 175 NSSGPYANGVYAGSTCOYSPFCEYSGHDSANGELMKNYF-----218
 DB 185 LTIAPYVKDVVILGSSGALGVRYLTAYDVKTGGVWRAYATGPKDLLADDEVKN 244
 QY 219 PRABEE-GEFTWNDYEARMTGA--WGOITDPTNLVHYSTAVCPASETORSTPG 273
 DB 245 AHYGKIGCTTWEGD--ANKIGGINWGMVAYDPGTNLIFETGNPAPANNETMR--PG 299
 QY 274 GLTGTNTRFAVRBDTGEIVMRHQTLPEDNDODECTEMMYTAVNOPSTEMEGLQSI 333
 DB 300 DNKM-TMTIFGRDADTGEAKFGYOKTPHDEWDYAGVNM-----PSEQKD-----344
 QY 334 NAATGERVLTGVCKTGTMMQFADGEELMAR--DTNNQNMIESIDENGIYVNEA 390
 DB 345 --KDKTKRLLTHPDNRNIYTLDTGALVSANKLDT--VNVFKYVDLTKGPPVNDPE 400
 QY 391 ILKELD-VEYDVCPTFLGGRMPSSALNPDGSIYFIPLNNVCYMMAVDOFTSMDYNT 449
 DB 401 YTRNDHLAKDYCPAMKYNHNGDSYPRKRELFPMGINHICMOWEPMLYRAGGFVVG 460
 QY 450 SNVTKLPKCK-----DMIGRIDALIDISTGRTLSVERAANAYSFVLSTGGGVLFNGSTD 503

DB 461 ATLNNYPCPKGRDQNYEGLQIKAYNATGSKYKWEKMERFAWCGTLATADLIVFGTLD 520
 QY 504 RYFRALSPFETITMOTFLATVASGOAISYEVDGMOYAI--AGGVSYG-----551
 DB 521 GYLKARSDTDGLMKFETPSGALGYPMPTYHKGTOYVAITYGVGNPGLVPLVDLDP 580
 QY 552 SGUNSLAGERV-DSTAIGNAVYFAL 577
 DB 581 AGLGAVGAFKRLANTYQGGGVIVFSL 607

RESULT 9
 ID DM1 METEX STANDARD; PRT; 626 AA.
 AC P16027;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE METHANOL DEHYDROGENASE SUBUNIT 1 PRECURSOR (EC 1.1.99.8) (MDH LARGE
 DE ALPHA SUBUNIT) (MDH).
 GN MOXF.
 OS Methylobacterium extorquens.
 OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
 CC Methylobacterium group; Methylobacterium.
 OX NCBI_TaxID=408;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=AM1 / NCIB 9133;
 RX MEDLINE=90337342; PubMed=2116368;
 RA Anderson D.J., Morris C.J., Nunn D.N., Anthony C., Lidstrom M.E.;
 RT "Nucleotide sequence of the Methylobacterium extorquens AM1 moxf and
 RT mox genes involved in methanol oxidation.";
 RL Gene 90:173-176(1990).
 RN [2]
 RP SEQUENCE OF 28-53.
 RC STRAIN=AM1 / NCIB 9133;
 RX MEDLINE=89350892; PubMed=2504152;
 RA Nunn D.N., Day D., Anthony C.;
 RT "The second subunit of methanol dehydrogenase of Methylobacterium
 RT extorquens AM1.";
 RL Biochem. J. 260:857-862(1989).
 RN [3]
 RP DISULFIDE BONDS.
 RX MEDLINE=95384759; PubMed=7656012;
 RA Blake C.C.F., Ghosh M., Harlos K., Avezoux A., Anthony C.;
 RT "The active site of methanol dehydrogenase contains a disulphide
 RT bridge between adjacent cysteine residues.";
 RL Nat. Struct. Biol. 1:102-105(1994).
 RN [4]
 RP X-RAY CRYSTALLOGRAPHY (1.94 ANGSTROMS).
 RX MEDLINE=95253818; PubMed=7735834;
 RA Ghosh M., Anthony C., Harlos K., Goodwin M.G., Blake C.;
 RT "The refined structure of the quinoprotein methanol dehydrogenase
 RT from Methylobacterium extorquens at 1.94 A.";
 RL Structure 3:177-187(1995).
 CC -1- CATALYTIC ACTIVITY: PRIMARY ALCOHOL + ACCEPTOR = ALDEHYDE +
 CC REDUCED ACCEPTOR.
 CC -1- COFACTOR: POO.
 CC -1- SUBUNIT: THE HOLOENZYME MDH HAS AN ALPHA-2/BETA-2 CONFIGURATION
 CC OF A LARGE ALPHA AND A SMALL BETA SUBUNIT.
 CC -1- SUBCELLULAR LOCATION: PERIPLASMIC, BUT ASSOCIATED WITH INNER
 CC MEMBRANE.
 CC -1- SIMILARITY: BELONGS TO THE BACTERIAL POO DEHYDROGENASE FAMILY.
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 CC

DR EMBL: M31108; AAA25380.1; .
 DR PIR: S07908; J00706.
 DR PIR: J00706; J00706.
 DR HSSP: P38539; 4AAH.
 DR InterPro: IPR001479; .
 DR InterPro: IPR002372; .
 DR Pfam: PF01011; Bacterial_PQQ_7.
 DR PROSITE: PS00363; BACTERIAL_PQQ_1; 1.
 DR PROSITE: PS00364; BACTERIAL_PQQ_2; 1.
 DR OxiReductase; PQQ; Signal; Methanol utilization; Periplasmic.
 FT SIGNAL 1 27
 FT CHAIN 28 626 METHANOL DEHYDROGENASE SUBUNIT 1.
 FT DISULFID 130 131
 FT DISULFID 413 442
 FT ACT_SITE 330 330
 SQ SEQUENCE 626 AA: 68434 MW: 64988DOAFDAD34C CRC64;

Query Match 15.2%; Score 468.5; DB 1; Length 626;
 Best Local Similarity 25.4%; Pred. No. 2.3e-25;
 Matches 159; Conservative 113; Mismatches 271; Indels 83; Gaps 23;

QY 10 SAGALALLA-AP-AFAQVYVTELLANPAGE-WISYQNGENRHSPLTQTENNQG 66
 DB 7 SVSALMALAPALSGAYANDKVELSKSDNWMVMPKNSNNSDLKQINKGNVAK 66
 QY 67 LQIYV--ARGMOGKVVPFLIDGVYKL--ANPDVICAIDAKTGDDLTMEHR-RQLPNI 121
 DB 67 LRAWTFSTELNGH-EGADLVVDGKMYHTSPNPFALGLDDPTTLIMQDPKONPAA 125
 QY 122 ATINSEPTRGMAIYGTN-----YFVSMNHLVALDTATQVTFEDVRCGEDEMVNS 175
 DB 126 RAVACCDLVNRGLAYVNGDGKTPALLKQLDGNVALNAEIGEYWKVKNENSIKRGSL 185
 QY 176 SSGPIYANGVIYAGSTQYSPFCEPVSCHDSATGEELMRYFT-----P 219
 DB 186 TIAPYVKKDKVILSSGAEIYGVYLTAVDKTGEQVWRAVATGPRKDLLASDFENIKRP 245
 QY 220 RAGEE--GDETMCNDYEARMTGA--WQIYDPTNIVHGSTAVGPASETORGTGG 274
 DB 246 HYGOKIGTGTWEGD--AMKIGGTTNMGVAYADPCTNLIYETGTPAPWNETMR--PGD 300
 QY 275 TLVGTTRRAVRPDGEIYWRHQTLPDWMDOCTPEMVTNVVQSTEMEGLSINPN 334
 DB 301 NKW-TWTIGRADTGEAFEGYKTPHDEM-----YAGVNVMLSEOKD----- 344
 QY 335 AATGERRVLTGVCKTGMQPDATGEELMAR--DTYQNMIESIDENGIVYVNEAI 391
 DB 345 -KDGKARKLLTHPDRNGIYITLIDRTGALVASAKLLDT--VNVFSSVDLKTGQVPARDPEY 401
 QY 392 LKELD-VEDYVCTFLGGRDWPSSALNPDGIVYFPLNVNVCYDMAVAVDQETSMDEVNTS 450
 DB 402 GTFMDHLADICPSANGYHNGHSDYDPKRELFFMGINICDMWEMFLPYRAGQEFVGA 461
 QY 451 NWTKLPPGK-----DMIRIDAIDISTGRTLSVERAANYSPVLSTGGVGLNGGTR 504
 DB 462 TLNMVPGPGDRQNYEGLOIKAYNAITGDYKWEKMERFAVWGTMATAGDILFYGLDG 521
 QY 505 YFRALSOETGLIMQRTLATVASGALISEVDGMQVAT--AGGVSYG-----S 552
 DB 522 YLKARDSDIGDLIMFKKIPSGAIGYPMYTHKGTQVAILYVGGMPGVGLVADLADPTA 581
 QY 553 GUNSLAGERV-DSTAIGNAVYVFAI 577
 DB 582 GLGAVGAFKKLANYTQMGGVVVFSL 607

RESULT 10
 ID DHML_METME STANDARD; PRT; 571 AA.
 AC P38539;
 DT 01-OCT-1994 (Rel. 30, Created)
 DT 01-OCT-1994 (Rel. 30, Last sequence update)

DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE METHANOL DEHYDROGENASE SUBUNIT 1 (EC 1.1.99.8) (MDH LARGE ALPHA
 OS SUBUNIT) (MEDH).
 OS Methylophilus methylotrophus (Bacterium W3A1).
 OC Bacteria; Proteobacteria; beta subdivision; Methylophilus group;
 OC Methylophilus.
 OX NCBI_TaxID=17;
 RN [1]
 RP X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS).
 RA MEDLINE=94059969; PubMed=8241148;
 RA White S., Boyd G., Mathews F.S., Xia Z.-X., Dai W.-W., Zhang Y.-F.,
 RA Davidson V.L.;
 RT "The active site structure of the calcium-containing quinoprotein
 RT methanol dehydrogenase.";
 RT Biochemistry 32:12955-12958(1993).
 RN [2]
 RP X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS).
 RX MEDLINE=93054513; PubMed=1331050;
 RA Xia Z.-X., Dai W.-W., Xiong J.-P., Hao Z.-P., Davidson V.L., White S.,
 RA Mathews F.S.;
 RT "The three-dimensional structures of methanol dehydrogenase from two
 RT methylotrophic bacteria at 2.6-A resolution.";
 RT J. Biol. Chem. 267:22289-22297(1992).
 CC -1- CATALYTIC ACTIVITY: PRIMARY ALCOHOL + ACCEPTOR = ALDEHYDE +
 CC REDUCED ACCEPTOR.
 CC -1- COPOLYMER: TWO MOLECULES OF PQQ AND TWO MOLECULES OF CALCIUM
 CC PER TETRAMER.
 CC -1- SUBUNIT: THE HOLOENZYME MDH HAS AN ALPHA-2/BETA-2 CONFIGURATION
 CC OF A LARGE ALPHA AND A SMALL BETA SUBUNIT.
 CC -1- SUBCELLULAR LOCATION: PERIPLASMIC, BUT ASSOCIATED WITH INNER
 CC MEMBRANE.
 CC -1- SIMILARITY: BELONGS TO THE BACTERIAL PQQ DEHYDROGENASE FAMILY.
 DR PDB: 4AAH; 08-DEC-96.
 DR InterPro: IPR001479; .
 DR InterPro: IPR002372; .
 DR Pfam: PF01011; Bacterial_PQQ_7.
 DR PROSITE: PS00363; BACTERIAL_PQQ_1; FALSE_NEG.
 DR PROSITE: PS00364; BACTERIAL_PQQ_2; 1.
 DR OxiReductase; PQQ; Methanol utilization; Periplasmic; 3D-structure;
 KM Calcium.
 FT DISULFID 103 104
 FT DISULFID 379 408
 FT ACT_SITE 297 297
 FT HELIX 2
 FT TURN 11 12
 FT STRAND 14 14
 FT TURN 17 18
 FT TURN 21 22
 FT STRAND 26 27
 FT TURN 34 36
 FT TURN 37 39
 FT STRAND 41 47
 FT STRAND 49 61
 FT TURN 59 63
 FT STRAND 62 63
 FT STRAND 64 68
 FT TURN 71 73
 FT STRAND 75 79
 FT TURN 80 81
 FT TURN 83 84
 FT STRAND 86 90
 FT STRAND 96 101
 FT HELIX 103 104
 FT TURN 103 104
 FT STRAND 112 114
 FT TURN 115 116
 FT STRAND 117 121
 FT TURN 123 124
 FT STRAND 126 131
 FT TURN 132 134
 FT STRAND 137 142
 FT TURN 146 148
 FT HELIX 149 149
 FT TURN 151 151
 FT STRAND 157 159

BASE (POTENTIAL).

"Characterization of the gcd gene from *Escherichia coli* K-12 W3110 and regulation of its expression.";
 J. Bacteriol. 175:568-571(1993).
 [3]
 RN SEQUENCE FROM N.A.
 RC STRAIN-K12 / W3110;
 RX MEDLINE=94261430; PubMed=8202364;
 RA Fujita N., Mori H., Yura T., Ishihama A.;
 RT "Systematic sequencing of the *Escherichia coli* genome: analysis of the 2.4-4.1 min (110,917-193,643 bp) region.";
 RL Nucleic Acids Res. 22:1637-1639(1994).
 [4]
 RN SEQUENCE FROM N.A.
 RC STRAIN-K12 / MG1655;
 RX MEDLINE=97426617; PubMed=9278503;
 RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Riley M., Collado-VIDES J., Glasner J.D., Rode C.K., Mayhew G.F., Mau B., Shao Y.;
 RT "The complete genome sequence of *Escherichia coli* K-12.";
 RL Science 277:1234-1238(1997).
 [5]
 RN TOPOLOGY
 RP MEDLINE=93286127; PubMed=8509415;
 RA Yamada M., Sumi K., Matsushita K., Adachi O., Yamada Y.;
 RT "Topological analysis of quinoprotein glucose dehydrogenase in *Escherichia coli* and its ubiquinone-binding site.";
 RL J. Biol. Chem. 268:12812-12817(1993).
 [6]
 RN 3D-STRUCTURE MODELING.
 RP MEDLINE=96128046; PubMed=8554505;
 RA Cozier G.E., Anthony C.;
 RT "Structure of the quinoprotein glucose dehydrogenase of *Escherichia coli* modelled on that of methanol dehydrogenase from *Methylobacterium extorquens*.";
 RL Biochem J. 312:679-685(1995).
 CC -1- FUNCTION: GDH IS PROBABLY INVOLVED IN ENERGY CONSERVATION RATHER THAN IN SUGAR METABOLISM.
 CC -1- CATALYTIC ACTIVITY: D-GLUCOSE + ACCEPTOR = D-GLUCONO-1,5-LACTONE + REDUCED ACCEPTOR.
 CC -1- COFACTOR: POO.
 CC -1- SUBUNIT: MONOMER.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. INNER MEMBRANE.
 CC -1- SIMILARITY: BELONGS TO THE BACTERIAL POO DEHYDROGENASE FAMILY.
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 CC -----
 DR EMBL: X51323; CAA35706.1; -
 DR EMBL: D12651; BAA02174.1; -
 DR EMBL: D26562; CAB20298.1; -
 DR EMBL: AE000122; AAC73235.1; -
 DR PIR: JVO107; JVO107.
 DR HSSP: P38539; 4AAH.
 DR ECGene: EG10369; gcd.
 DR InterPro: IPR001479; -
 DR InterPro: IPR002372; -
 DR Pfam: PF01011; Bacterial_POO_7; 7.
 DR PROSITE: PS00363; BACTERIAL_POO_1; 1.
 DR PROSITE: PS00364; BACTERIAL_POO_2; 1.
 KW Oxidoreductase; POO; Transmembrane; Cytoplasmic.
 FT DOMAIN 1 10
 FT TRANSMEM 11 37
 FT DOMAIN 38 40
 FT TRANSMEM 41 58
 FT DOMAIN 59 62
 FT TRANSMEM 63 81
 FT DOMAIN 82 95
 FT PERIPLASMIC (PROBABLE).

FT TRANSMEM 96 110 PROBABLE.
 FT DOMAIN 111 118 CYTOPLASMIC (PROBABLE).
 FT TRANSMEM 119 141 PROBABLE.
 FT DOMAIN 142 146 PERIPLASMIC (PROBABLE).
 FT ACT SITE 466 466 BASE (PROBABLE).
 FT CONFLICT 59 59 R -> L (IN REF. 1).
 FT CONFLICT 149 156 TUSADATP -> HLKRRCHT (IN REF. 1 AND 2).
 FT CONFLICT 193 193 N -> K (IN REF. 1 AND 2).
 FT CONFLICT 666 666 Q -> H (IN REF. 2).
 SQ SEQUENCE 796 AA; 86747 MW; D9EDC05A12894E9 CRC64;

Query Match 12.7%; Score 392.5; DB 1; Length 796;
 Best Local Similarity 24.3%; Pred. No. 6.5e-20;
 Matches 179; Conservative 85; Mismatches 231; Indels 241; Gaps 36;

QY 6 LWAS-----AGALALAPAFQOVPTPELLANPAGEMISYGNQENYRHSPLTQ 58
 DB 135 LTMAGFNDOEINGTISADATPAEA-ISPVDQ-----DMPAYGRNDSQRFSPILKQ 185
 QY 59 ITTENYQQLQLVYA-----RGMPGRKY--QVTEPLIHGVYLYANPGDVIQADAKTGD 109
 DB 186 INADYHNHLEAMVFTGPDYKQPNPDGETTNEVTEPIKQDITLYCTAHQRFLDALDAAGK 245
 QY 110 LIMEHRRQPLNATLNSPEEP--RGALYGTNVFVS-----WQNHLYAL 153
 DB 246 EKMHD--PELTNBSFHVTCRGVSHEAKAETASPEWADCPRIILPVDRLAI 302
 QY 154 DPTAGOV--TF-----DVRGQGEDMYSNSSGPIVANGVIT-AGS--TCQYS- 195
 DB 303 NANGKLCETFAKNGVLYNLSMMPDKG---LKEPISPIITDKITVMAGSTVDNST 358
 QY 196 -EPGCVSHSDATGEELRNFTFRA-----GEEDDEFWQNDYKARMGTGAGQITTY 247
 DB 359 RETSGVIRGEFVNTGTELLWA--FDGAKDPNAPISDEFTFFNS-----PNSAPAPAY 409
 QY 248 DPTNIVHYGSAVGPASPTGRTGPGTLYGNTREFAVRPPDGETLWYRHOTLPDNDQD 307
 DB 410 DAKLDLYIIPKQVTPPDWIGNKRTEBOERYAST-LALNATTKLANSYQVYHNDLMD 468
 QY 308 CTFEMVATNVQVSTEMEGLOSINPNAATGERRVLTGVPCKTGMQFPAETGEFL--- 364
 DB 469 -----LPAQPT-----LADITVN--GQKVVIYAPAKTGNIFFLDNRGELVYA 511
 QY 365 -----WARDNYQNMIESIDENCI-----VYNEDALIKEL--DVEYD-- 400
 DB 512 PEKVPQGAAGDYVTPQPPSELSFRPTKDLSGADMGATMFDQLCVRFHQRREGI 571
 QY 401 -----VCPFLGGRDWPSSALNP----- 418
 DB 572 FTTPSEQGTIVFGSLGFMFENGGISVDNREVALIANPALFVSKLIPRGGNPMQPKD 631
 QY 419 -----DSGI-----YFIPLVNVCYDMAVDOEFTSMQVYNTSNVTKLPPGKDMIGRI 465
 DB 632 AKGTGTESGIQPOYGVPPYVTLN-----PFLS-----PFGJPCPKPANGYI 672
 QY 466 DAIDISTGRTLSVERAANANS-----PY-----ISTGGVFNFGCT--DRY 505
 DB 673 SALDKTNEVYWKRIKIPQDSMPFPMFVPPFMKMGPHLGGIPSTAGVLETAATADNY 732
 QY 506 FRALSQETGETLMQTRLATVASSGA--ISYEDVMQYVAI-AGGGVSYSGSLNSALAGER 562
 DB 733 LRAVMSNGEKLMOGRLLP--AGGATPMTEVNGKQVYVVISAGHSGSFG----- 779
 QY 563 VDSIRAGNAVVEPALP 578
 DB 780 ---TKMGDIYVYALP 792
 RESULT 12
 ID DHGA_ACICA STANDARD; PRT; 801 AA.
 AC P05465;

DT 01-NOV-1988 (Rel. 09, Created)
 DT 01-NOV-1988 (Rel. 09, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE GLUCOSE DEHYDROGENASE-A [PYRROLOQUINOLINE-QUINONE] PRECURSOR
 DE (EC 1.1.99.17) (QUINOPROTEIN GLUCOSE DH) (GDH-A).
 GN GDH.
 OS Acinetobacter calcoaceticus.
 OC Bacteria; Proteobacteria; gamma subdivision; Moraxellaceae;
 OC Acetobacter.
 OX NCBI_TaxID=471;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=LM2 79.41;
 RX MEDLINE=86289368; PubMed=3399393;
 RA Cleton-Jansen A.-M., Goosen N., Odle G., van de Putte P.;
 RT "Nucleotide sequence of the gene coding for quinoprotein glucose
 dehydrogenase from Acinetobacter calcoaceticus."
 RL Nucleic Acids Res. 16:6228-6228(1988).
 CC -1- CATALYTIC ACTIVITY: D-GLUCOSE + ACCEPTOR = D-GLUCONO-1,5-LACTONE +
 + REDUCED ACCEPTOR.
 CC -1- COFACTOR: POO.
 CC -1- SUBUNIT: MONOMER.
 CC -1- SUBCELLULAR LOCATION: PERIPLASMIC.
 CC -1- MUSCELLAROUS: ACINETOBACTER CALCOACETICUS CONTAINS TWO DIFFERENT
 POO DEPENDENT ENZYMES WITH GDH ACTIVITY. GDH-A PREFERENCES
 2-DEOXYGLUCOSE AS SUBSTRATE, THE SPECIFIC SUBSTRATES FOR GDH-B ARE
 DISACCHARIDES.
 CC -1- SIMILARITY: BELONGS TO THE BACTERIAL POO DEHYDROGENASE FAMILY.
 CC
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 or send an email to license@isb-sib.ch).
 CC
 DR EMBL; X07235; CAA30222.1; -;
 DR PIR; S00943; S00943.
 DR InterPro; IPR001479; -;
 DR InterPro; IPR002372; -;
 DR Pfam; PF01011; Bacterial_POO_7.
 DR PROSITE; PS00363; BACTERIAL_POO_1; 1.
 DR PROSITE; PS00364; BACTERIAL_POO_2; 1.
 KM Oxidoreductase; POO; Transmembrane; Periplasmic; Signal.
 FT SIGNAL 1 ?
 FT CHAIN ? 801
 FT TRANSMEM 39 55
 FT TRANSMEM 59 79
 FT TRANSMEM 94 108
 FT TRANSMEM 119 138
 FT ACT SITE 471 471
 SEQUENCE 801 AA; 86956 MM; 2F4E222E5450D8 CRC64;
 Query Match 12.6%; Score 390; DB 1; Length 801;
 Best Local Similarity 23.4%; Pred. No. 9.8e-20;
 Matches 169; Conservative 88; Mismatches 226; Indels 240; Gaps 33;
 QY 20 PAFQAVPYVDELANPPAGMISYIGONQENYRSLPTQTTEVNGQLVMARQMPGK 79
 DB 152 PETAQAVPGVAE-----SDMPAYGRTQAGVRSPLKQINDQVKKLAWMT--LRTGD 202
 QY 80 V-----QVTPLIHGVMTLANPGBVIOAIDAKTGDLMEHRRQLPNTATLSFG 128
 DB 203 LKTNDSELTNTQVTKIKIGNMFTCTAHOQLAIDATGKPKK--RDPKLTGKSFQ 239
 QY 129 EPT-EGMALYGTN-----VYFVSMNHLVALDPTATGQVTFVDV 165
 DB 260 HLTGRGVYDANNTTEFANSLSQSKSSSTQCPKRVFVPPVNDGRLVAVNDTGACTDFG 319
 QY 166 RGQGDWMS-----NSSGPVANGVIVAGS--TCQYS---PFGFVSHDSATG 209

DB 320 QMGVNLQEFMPYAPPGYNPTSPGIYTGSTVIVAGSVNTNYSNKEPSG-VIRGYDVNTG 378
 QY 210 EELMRNFETFRAGE-----EGDETWNDEYARMNTGAMQILYDPTNLVHGSNAYGP 263
 DB 379 KLMV--VFDTGADPNAMPBEGTTFVHNS-----PNAMPVLAIDAKLDIV-VVPTGV-- 427
 QY 264 ASETORCTPGGTLYG-----TNTREAVRDEGEIYWRHQTLPDRNDQECTFEEM 313
 DB 428 -----GTP--DLWGDRTLEKERYANSMLAINASGKLVWNNQTHHDLMDNDVDSQPS 479
 QY 314 VTNVDPVPTSTEMEGLOSINP--NAATGERVLTGPV-----CKTG--TMQFDP 357
 DB 480 LADIKNKAGQTVPAIVLTGTGNAFVLDNR--NGQPIVPTERPVQTVKRGQPTGGEFY 537
 QY 358 AENGEF-----LMA-----ROTNYNQMIESIDENGIYVNVND 389
 DB 538 SKTQPSFDLMLAQDQLTKDKMMGATMLDQLMCRVSRFLNYGITYPSENGTL----- 592
 QY 390 ALIKELDEVYDVCPTFLGCRDMPSAALNPS-----GIYFI----- 425
 DB 593 -----VFGNIGVEFMGMSVNPDRQVAVNMPISGLPFSVRLIPADPNRAQTAG 641
 QY 426 -----PLNNVCYDMAVDOEFTSMDYNTSNVTKLPPEKDMIGRIDALISTGRTLM 477
 DB 642 AGTEQGVQPMYGVY-----GVEISAFSLPLGLPCKQPMAGYVAGVDLKTHEVVM 691
 QY 478 -----SYERAANYSPLYSTGGGVLPNGGT-DKYPALSOETGETLM 518
 DB 692 KRRTIGTRDSLPMLFQPLPAGVIGVPGIGSISTAGVAMFVAGVADVYLRFAVNTNKKML 751
 QY 519 QTRLATVAGSQA--ISEYVDGMQYVAI-AGGGSYSGLNSALAGBRVSTAGNAVYVF 575
 DB 752 EALHP--AGGQATIPMYTEINGKQYVIMAGGHSFG-----TKMGDVLAVY 795
 QY 576 ALP 578
 DB 796 ALP 798
 RESULT 13
 DHG_GLUOX STANDARD; PRT; 808 AA.
 AC P27175;
 DT 01-AUG-1992 (Rel. 23, Created)
 DT 01-AUG-1992 (Rel. 23, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE GLUCOSE DEHYDROGENASE [PYRROLOQUINOLINE-QUINONE] PRECURSOR
 DE (EC 1.1.99.17).
 GN GDH.
 OS Gluconobacter oxydans.
 OC Bacteria; Proteobacteria; alpha subdivision; Acetobacteraceae;
 OC Gluconobacter.
 OX NCBI_TaxID=442;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92017653; PubMed=1833618;
 RA Cleton-Jansen A.-M., Dekker S., van de Putte P., Goosen N.;
 RT "A single amino acid substitution changes the substrate specificity
 of quinoprotein glucose dehydrogenase in Gluconobacter oxydans."
 RL Mol. Gen. Genet. 229:206-212(1991).
 RN [2]
 RP REVISION TO 213.
 RA Goosen N.;
 RL Submitted (FEB-1992) to the EMBL/Genbank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: D-GLUCOSE + ACCEPTOR = D-GLUCONO-1,5-LACTONE +
 + REDUCED ACCEPTOR.
 CC -1- COFACTOR: POO.
 CC -1- SUBCELLULAR LOCATION: OUTSIDE OF THE PERIPLASMIC MEMBRANE.
 CC -1- MISCELLANEOUS: THE P1 FORM CAN OXIDIZE ONLY D-GLUCOSE, WHILE THE
 P2 FORM CAN ALSO OXIDIZE MALTOSE. THE SEQUENCE OF P1 FORM IS SHOWN
 HERE.
 CC -1- SIMILARITY: BELONGS TO THE BACTERIAL POO DEHYDROGENASE FAMILY.

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 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
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 CC or send an email to license@sib-sib.ch).

DR EMBL: X62710; CAA44594.1; ALT_SEQ.
 DR PIR: S17716; OPKEX.
 DR InterPro: IPR001479; -
 DR InterPro: IPR002372; -
 DR Pfam: PF01011; Bacterial_PQO_7.
 DR PROSITE: PS00363; BACTERIAL_PQO_1; 1.
 DR PROSITE: PS00364; BACTERIAL_PQO_2; 1.
 KW Oxidoreductase; PQO; Transmembrane; Periplasmic; Signal.
 FT SIGNAL 1 219
 FT CHAIN 720 808
 FT TRANSMEM 35 54
 FT TRANSMEM 59 76
 FT TRANSMEM 94 108
 FT TRANSMEM 123 138
 FT ACT SITE 470 470
 FT VARIANT 788 788 H -> N (IN P2 FORM).
 SQ SEQUENCE 808 AA: 87567 MW: 0F4160DA78652445 CRC64:

Query Match 11.0%; Score 340; DB 1; Length 808;
 Best Local Similarity 21.8%; Pred. No. 3.1e-16;
 Matches 159; Conservative 98; Mismatches 259; Indels 212; Gaps 30;

QY 13 ALALLAARFAOVTPTDELIA-----NPPAGEWISYGGONGEYRHSPLTQITTT 61
 DB 128 AVLAFAFASLFTDPHDISGLPTQIINASPADPDNVPASMAHYGRTQAGDRMSPLNOINA 187
 QY 62 ENVGOLQLW-----ARGMOPGV--OVTPLIHDGVVYLANPDVIOAIDAKGDLIM 112
 DB 188 TIVSNLKVAMHHTKIDMANSNDPGEITNATPIEFNNITLYMGLSKLOKLEAVDGAAGANKW 247
 QY 113 EHRROD--PNTATLN---SFGC--PTRGMALYGT-----NVEFVSDNHLVALDT 155
 DB 248 YVDPKLIQINPFOHLCRCGVSEHETPANAMSDGNAPFDCAKDSILLPVN--DGRLEVEDA 306
 QY 156 AIGQVTEVD--DNGGEGEDMSN-----SSGPIYANGIYVA-----GSCQYSP 196
 DB 307 DTGKTCGFGNGGEIDLRVNPQPYTTPGQYEPTSPVITDKLILANSATIDNGSVKQASG 366
 QY 197 FCGFVSGHDSATGEELM---RNYFIPRAGEGDETWGNDYFARMWTGAMQITVDPTVN 252
 DB 367 ---ATGAFVYTGKRWYVDASNPBPNOJLPDSHFVHNHNSNSMIVS---STDANLN 418
 QY 253 LVHYGSFVAVGAPASETGRT---GGTLVGTNTRF---AVRPDTGEIYVWRHQLPRDNW 304
 DB 419 LVYIPMGV-----GTRDQMGGRDRTKDSERFAAGIALNALNADKLAMFYQYVHNDLM 469
 QY 305 DOBCFEMAVTVNDVOPSTREMEGLDGINNATGERRVLTGVPCKTGTMMQDADATG--EF 363
 DB 470 DMELPQSLVLDVYTKDGLVPAIYA-----PRTYTGDIFFVLDRTGKEI 513
 QY 364 LVARDT-----NYQMIESIDENGIVVNEDAILKELDV----- 397
 DB 514 VARPEIPVQGAAPGDHSTPTQPMQO---LTLRPKNPLNDSDINGTIFDQMFCSIYFHT 570
 QY 398 -EYD-----VCPFLGGRDWPASALNPSGIYFPLNVCYDMAVDO----- 439
 DB 571 LREGEFTPPSLKSLIFPGDGMFEMGLAVDPQROVAFANPISLPFVSQLVPRGPNP 630
 QY 440 -----EFTSMDEVYNTSNVTKLPPGKDMT-----GIDAIDIST 472
 DB 631 LWPENAKGTGETGLQHNHYGIPAVVNLHPFLDPLLFPFGIMPCRTPTPMGWVAGIDIKT 690

QY 473 GRTLSVERAANYS-----PV-----LSTGGVLP-NGGTDYRFALS 510
 DB 691 NKVWQHRNGTLDKRDMSGLSLPIPLPIKIGVPSLGSPSTANGLFTRASNDYIRAVN 750
 QY 511 QETGETLMQTRLATVASGAQISYEVDMQVAYAGGVSYGSLNSALAGERVDAITGN 570
 DB 751 LTTGKVLMDORLPAGAQATETFYAINGKQYI-----VTVAGGNSF-----PTRMD 797
 QY 571 AVYVFALP 578
 DB 798 DIALYALP 805

RESULT 14
 QUIT_ACTICA STANDARD; PRT; 809 AA.
 ID QUIT_ACTICA
 AC Q59086;
 DT 01-OCT-2000 (Rel. 40, Created)
 DT 01-OCT-2000 (Rel. 40, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE QUINATE/SHIKIMATE DEHYDROGENASE [PYRROLOQUINOLINE-QUINONE]
 DE (EC 1.1.99.25) (MAD(P)-INDEPENDENT QUINATE DEHYDROGENASE).
 GN QUITA.
 OS Acinetobacter calcoaceticus.
 OC Bacteria; Proteobacteria; gamma subdivision; Moraxellaceae;
 OC Acinetobacter.
 OX NCBI_TaxID:471;
 RN [1]
 RP SEQUENCE FROM N.A., AND CHARACTERIZATION.
 RC STRAIN-BD143 / ADPL;
 RA MEDLINE:95095936; PubMed-8002591;
 RX Elsmore D.A., Ornston L.N.;
 RT "The pca-pob supraoperonic cluster of Acinetobacter calcoaceticus
 RT contains quia, the structural gene for quinate-shikimate
 RT dehydrogenase.";
 RL J. Bacteriol. 176:7659-7666(1994).
 RN [2]
 RP SEQUENCE OF 1-20 FROM N.A.
 RC STRAIN-BD143 / ADPL;
 RX MEDLINE:96011389; PubMed-7592351;
 RA Elsmore D.A., Ornston L.N.;
 RT "Unusual ancestry of dehydratases associated with quinate catabolism
 RT in Acinetobacter calcoaceticus.";
 RL J. Bacteriol. 177:5971-5978(1995).
 CC -1- FUNCTION: CAN ACT EITHER ON QUINATE OR ON SHIKIMATE.
 CC -1- CATALYTIC ACTIVITY: QUINATE + PYRROLOQUINOLINE-QUINONE = 5-
 CC DEHYDROQUINATE + REDUCED PYRROLOQUINOLINE-QUINONE.
 CC -1- CATALYTIC ACTIVITY: SHIKIMATE + PYRROLOQUINOLINE-QUINONE - 3-
 CC DEHYDROSHIKIMATE + REDUCED PYRROLOQUINOLINE-QUINONE.
 CC -1- COFACTOR: PQO.
 CC -1- PATHWAY: QUINIC ACID CATABOLIC PATHWAY; FIRST STEP. THIS PATHWAY
 CC ALLOWS GROWTH OF BACTERIA WITH QUINATE BY ITS CONVERSION TO
 CC PROTOCATECHUATE AND SUBSEQUENT METABOLISM BY THE BETA-KETOADIPATE
 CC PATHWAY.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
 CC -1- INDUCTION: BY PROTOCATECHUATE.
 CC -1- SIMILARITY: BELONGS TO THE BACTERIAL PQO DEHYDROGENASE FAMILY.
 CC -----
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 CC or send an email to license@sib-sib.ch).

DR EMBL: L05770; AAC37161.1; -
 DR Pfam: PF01011; Bacterial_PQO_7.
 DR PROSITE: PS00363; BACTERIAL_PQO_1; FALSE NEG.
 DR PROSITE: PS00364; BACTERIAL_PQO_2; FALSE NEG.
 KW Oxidoreductase; PQO; Quinate metabolism; Transmembrane.
 FT TRANSMEM 14 34
 FT TRANSMEM 41 61
 FT POTENTIAL.

FT TRANSMEM 68 88 POTENTIAL.
 FT TRANSMEM 90 110 POTENTIAL.
 FT TRANSMEM 127 147 POTENTIAL.
 SQ SEQUENCE 809 AA; 88196 MW; 71F67CEBA62BFCB CRC64;

Query Match 10.18; Score 313.5; DB 1; Length 809;
 Best Local Similarity 23.38; Pred. No. 2.2e-14;
 Matches 160; Conservative 80; Mismatches 262; Indels 185; Gaps 26;

3 PTSLMASAGALLAA--PAFAQYPTVDELAMPAGEWISYQONENRHSPLQITTT 61
 148 PHEVTKASGEELPLVPVDPKAKQY-----NMDDHGNDAAGSREVALDQINR 193
 62 ENVSQLOLVW-----ARGMOPG-KYQVTPPLHDGVYLANPGDVLOADAKTDLIME 113
 194 NNVEKIKAMFRRTGDTTGTGNGAEDOMPTLOYKNKVFLLCTPHNNLFAIDADSGKQIMK 253
 114 HRROLPIATLINSFG--EPTRGMAIYGT-----NVEYV 144
 254 -----AEVNSTADAMERCRGVAEFDSTQPLVQPTLAGATPAALAAANTECPRRYTN 305
 145 SMDHVALDPAFG-----QYTFVDNQGQEDMYSN-----SSGPIVANGVIAGSTC 192
 306 TVDRLIAVNDATGACRCKDGVNCTVNLHGLGENTKAPREVTASPTIAGTTIIVGSRI 365
 193 QYSPF-----GCVFSGHDSATGEELMRYNFIIPRAGEEDETGMNDYEARMWTGAMGQITTD 248
 366 ADVNAADMPGGVIRAYVITIGKLFMA--FPPRNDPPIVYAKPGIYKRSSTNSMAASTYD 423
 249 PVTPLVH--YGSTAVGASSETQRTPGCTLYGINTFAVRPDGELIYWHQTLPRDNWDQ 306
 424 PDMTIVFLPMGSSSVDVWGGNR--TAADHKYNTSV-LALATATGKEKVVNTVHNDLMD- 479
 307 ECTPEMWTNVDPQSTEMEGLOSINPNAATGERRVLTGVCRTGTMWGDAETGEEL-- 364
 480 -----FDLPMPQS-----LVDFPMKDDTTPKAVVIGT--KSGQFVLDRAVTKPLIK 524
 365 -----WARDNTYONMIESIDENGIVYNE-----DALIKELD--VEYD 400
 525 VIEPIKVIADIPRGYQSKTQPRSVEMPQIGNOTLKESDMGAGPFDQLMKRNPKSRYD 584
 401 -----VCPITLGGHDMPSAALNDSCITF-----IPL 427
 585 GLYTPAGTIVSLSEPPSISGGMNMGSIADFPTHRMYFVNDMRILGLIOTLIKOTPEDIKIOA 644
 428 N---NVCYDMAAVDQDEFTSMDYNTSNVTKL--PRGKDMIGRIDAIDISGRILWSYERA 482
 645 NGGEKVTMGGAIVPMKGTPIYKVNKNRPMASALGIPCCQPPFGTMTALIDMKTRQYAAWQVPLG 704
 483 AANYS-----PVLSTGGGVLENGGTDYFRALSOETGETLMQTRL 522
 705 TIDGTGPMGIKMGLKAPIGMTPTGGPMATGGGLVFPAATQDYLLRAFNSSNGEIMKARL 764
 523 ATVASQAISY--EVDGMYVAIAGG 547
 765 PVSGGTPMSTYMSKPTGKYVYVVSAGG 791

RESULT 15
 QUITA_XANCUJ STANDARD; PRT; 790 AA.
 AC Q9XD78;
 DT 01-OCT-2000 (Rel. 40, Created)
 DT 01-OCT-2000 (Rel. 40, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE PROBABLE QUINATE DEHYDROGENASE [PYRROLOQUINOLINE-QUINONE]
 DE (EC 1.1.99.25).
 GN QUMA.
 OS Xanthomonas campestris (pv. juglandis).
 OC Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;
 NC Xanthomonas.
 NCBI_TaxID=44291;

RN [1]
 RC SEQUENCE FROM N.A.
 RC STRAIN=C5;
 RX MEDLINE=20063481; PubMed=10594704;
 RA Lee Y.-A., Lo Y.-C., Yu P.-P.;
 RT "A gene involved in quinate metabolism is specific to one DNA homology
 group of Xanthomonas campestris";
 RL J. Appl. Microbiol. 87:649-658(1999).
 CC -1- CATALYTIC ACTIVITY: QUINATE + PYRROLOQUINOLINE-QUINONE = 5-
 CC DEHYDROQUINATE + REDUCED PYRROLOQUINOLINE-QUINONE.
 CC -1- COFACTOR: PQO (BY SIMILARITY).
 CC -1- PATHWAY: QUINIC ACID CATABOLIC PATHWAY; FIRST STEP. THIS PATHWAY
 CC ALLOWS GROWTH OF BACTERIA WITH QUINATE BY ITS CONVERSION TO
 CC PYRROLOQUINOLINE-QUINONE.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
 CC -1- SIMILARITY: BELONGS TO THE BACTERIAL PQO DEHYDROGENASE FAMILY.
 CC
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 CC
 CC EMBL: AF109471; AAD38453.1;
 CC Pfam: PF01011; Bacterial_PQO_6.
 CC DR PROSITE: PS00363; BACTERIAL_PQO_1; FALSE_NEG.
 CC DR PROSITE: PS00364; BACTERIAL_PQO_2; FALSE_NEG.
 CC KW Oxidoreductase; PQO; quinate metabolism; Transmembrane.
 FT TRANSMEM 22 42 POTENTIAL.
 FT TRANSMEM 48 68 POTENTIAL.
 FT TRANSMEM 77 94 POTENTIAL.
 FT TRANSMEM 106 126 POTENTIAL.
 SQ SEQUENCE 790 AA; 82896 MW; B75F29B52449E6F CRC64;

Query Match 8.98; Score 276; DB 1; Length 790;
 Best Local Similarity 22.18; Pred. No. 8.7e-12;
 Matches 164; Conservative 79; Mismatches 262; Indels 226; Gaps 33;

9 ASAGALALLA--APAFQYPTVDE--LIANPAG--EMISYQONENRHSPLQI 59
 110 ATVALAVALVAGIGMEVPHPVAGNAPGMTAVPGSVQOAMSAYGNDGSGRFAALDI 169
 60 TIENSGOLOLVNARGQPEKV-----QVTPLIHDGVYLANPGDVLOADAKTD 109
 170 NRSN--GRPAAGSPGPTTPEIANSNGAEDQTLPLQVEKVFLLCTPHNNLIALDASTGK 228
 110 LIWEHRROLPIATLINSFCEPTRGMALY-----GTN-----V 141
 229 QLM--RRE--INATSSVWQRCRGICYPADAAALAPSVANSPILAAVYVAGANCRRRL 283
 142 YFVSWDNLVALDTAT-----GQYTFVDNQGQED--MVSNSGPIVANGVIAGS 190
 284 FNTTIDGRILVADDTGAFCQGFSGNGQVDLKAAGLAAPDEPYQLTSPVAGTIVGGR 343
 191 T-----CQSPRCGCVFSGHDSATGEELMRYNFIIPRAGEEGDGTWENDE-----A 235
 344 TRADDNVQTDMPGVAVRG-----SMWSP--VRSAGLDP-----GNPHDROAPAAGSSIV 390
 236 RMMTGAMGQITVDPVYTNLVHGSTAVGPASFTQRTPGCTLYGTN-----TRPAV 285
 391 RSTPNNVMAKMSYDAAMNYF-----LPLGGPSTDLGARTALDHRYGASVIAL 439
 286 RPDGTGEIYWHQTLPRDNWDQCTFEEMVNTVNDVQSTEMEGLOSINPNAATGERRVLTG 345
 440 DATGAEKVVQTYVHNDLMD-----FDLPMPQS-----IDPPNDGSGHTPAVV 483
 346 VCKCTGTMQGPAAETGEFLW--ARDT-----NY--QNMIESIDENGIVYNEPAI 391
 484 IGTGAGQIYVLDRAVTKPLTEVEVPVKGSIDIAHQYAPTPQLVSGMPOIGTKHLTSDM 543

```

QY 392 LKELDEVYDVC-----PTFLGGRDMPSSAALNPDSGIYF--- 424
      : : : : : : : : : : : : : : : : : : : : : :
Db 544 WGTAMDQMLCRIAFAKQMRKEGLYAPGTDVLSFPGSLGGMMGGLSTDVPHDVVFAND 603
      : : : : : : : : : : : : : : : : : : : : : :
QY 425 -----IPLNN-----VCYDMMAVDOFTSMDEVYNTSNVTKL-----PG 458
      : : : : : : : : : : : : : : : : : : : : : :
Db 604 MRLGLWQMTIPADTRKAEAGGGEAVNTGMGAVPLKGTPIYAVNKNRFLSALGIPCQARP- 662
      : : : : : : : : : : : : : : : : : : : : : :
QY 459 KDMIGRIDAIDISTGRTLMSVERAAN-----YSPV-----ISTGGVLEFN 499
      : : : : : : : : : : : : : : : : : : : : : :
Db 663 ---YGTLSAIDIKTRSIAMQYVGVODTGPFGIKMHLPIPIGMPTLGTLSTOGGLVEI 719
      : : : : : : : : : : : : : : : : : : : : : :
QY 500 GGT-DRYPRALSQETGELTMOFLATVASGAISY--EVDGMQYVAIAGGVSYSGSLNS 556
      : : : : : : : : : : : : : : : : : : : : : :
Db 720 AGTQDYLERAFDSATGKELMKGRLPVGSOGPIITYVSHKTKQYVVISAGGAR----- 772
      : : : : : : : : : : : : : : : : : : : : : :
QY 557 ALAGERVDSTAIGNAVYVFPALP 578
      : : : : : : : : : : : : : : : : : : : : : :
Db 773 -----QSPDRGDYVIAVSLP 787
      : : : : : : : : : : : : : : : : : : : : : :

```

Search completed: August 8, 2001, 19:44:11
 Job time: 183 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 8, 2001, 19:40:38 ; Search time 27.61 Seconds
(Without alignments)
2774.524 Million cell updates/sec

Title: US-08-934-506A-5

Sequence: 1 MKPSTLWASGALALALAP.....GERVDSFAGNAVVFALPQ 579

Scoring table: BLOSOM62
Gapop 10.0 , Gapext 0.5

Searched: 425026 seqs, 132305027 residues

Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

SPREMBL_16:*
1: sp.archaea:*
2: sp.bacteria:*
3: sp.fungi:*
4: sp.human:*
5: sp.invertebrate:*
6: sp.mammal:*
7: sp.mhc:*
8: sp.organelle:*
9: sp.phage:*
10: sp.plant:*
11: sp.podent:*
12: sp.unclassified:*
13: sp.vertebrate:*
14: sp.virus:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	616	19.9	698	2	Q9KH03
2	583	18.9	708	2	Q46444
3	561	18.2	742	2	053362
4	560	18.1	601	2	09EYW8
5	549.5	17.8	695	2	Q9F9U2
6	537.5	17.4	601	2	P71509
7	479.5	15.5	633	2	024759
8	473	15.3	599	2	Q9L935
9	439.5	14.2	573	2	059540
10	365.5	11.8	790	2	09X255
11	327	10.6	803	2	Q9L115
12	324.5	10.5	786	2	P95466
13	281.5	9.1	644	2	Q52551
14	276.5	9.0	639	2	P77931
15	218	7.1	470	2	030326
16	208.5	6.7	182	2	032699
17	203.5	6.6	179	2	032697
18	200.5	6.5	180	2	032700
19	200.5	6.5	180	2	032696

20	200.5	6.5	181	2	032615	hypomicrob
21	199.5	6.5	181	2	032692	hypomicrob
22	197.5	6.4	181	2	032703	hypomicrob
23	196.5	6.4	181	2	032621	hypomicrob
24	195.5	6.3	182	2	032706	hypomicrob
25	193.5	6.3	180	2	032701	hypomicrob
26	191.5	6.2	182	2	032612	hypomicrob
27	191.5	6.2	184	2	032693	hypomicrob
28	190.5	6.2	172	2	033894	hypomicrob
29	186.5	6.0	172	2	033882	hypomicrob
30	186.5	6.0	179	2	032707	hypomicrob
31	185.5	6.0	180	2	032704	hypomicrob
32	185.5	6.0	180	2	032694	hypomicrob
33	185	6.0	171	2	033884	hypomicrob
34	183.5	5.9	179	2	032702	hypomicrob
35	182.5	5.9	184	2	032695	hypomicrob
36	181.5	5.9	185	2	0918K8	uncultured
37	174.5	5.6	179	2	032698	hypomicrob
38	172.5	5.6	185	2	0918L0	uncultured
39	169.5	5.5	185	2	0918K9	uncultured
40	169	5.5	499	2	051842	thiodacillu
41	168.5	5.5	172	2	033889	unidentifite
42	168.5	5.5	172	2	09FDE8	unidentifite
43	167.5	5.4	172	2	033886	unidentifite
44	167.5	5.4	407	1	027529	methanobact
45	167.5	5.4	524	2	Q9PB85	xyliella fas

ALIGNMENTS

RESULT 1
ID Q9KH03 PRELIMINARY: PRT; 698 AA.
AC Q9KH03;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TReMBLrel. 16, Last annotation update)
DE TERAHYDROFURFURYL ALCOHOL DEHYDROGENASE.
OS Alcaligenes eutrophus (Ralstonia eutropha).
OC Bacteria; Proteobacteria; beta subdivision; Ralstonia group;
OC Ralstonia.
OX NCBI_TaxID=510;
RN [1]
RP SEQUENCE FROM N.A.
RA Zarrat G., Schraeder T., Andreessen J.;
RT "Molecular analysis of PQQ-dependent THFA-DR.;"
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF277373; AAF86335.1; -.
DR InterPro: IPR000345; -.
DR InterPro: IPR002372; -.
DR InterPro: IPR003088; -.
DR Pfam: PF000034; cytochrome c; 1.
DR Pfam: PF01011; Bacterial PQQ; 6.
DR PROSITE: PS00190; CYTOCHROME C; UNKNOWN_1.
DR PROSITE: PS00190; CYTOCHROME C; UNKNOWN_1.
SQ SEQUENCE 698 AA: 75471 MW: 9C87F180DB1D2FB2 CRC64;

Query Match 19.9%; Score 616; DB 2; Length 698;
Best Local Similarity 30.3%; Pred. No. 2, 8e-35;
Matches 186; Conservative 93; Mismatches 247; Indels 88; Gaps 25;
QY 10 SAGALALIALAPAPA--OVTPVDELLANPPAG--EWISYQONENRHSPLTOITTEBNG 65
DB 14 AAASVALPAPMAFGANAARVDGAIRANBAGTPNMPSTGLDYAEFTFSKLEQVNGNVR 73
QY 66 QLOLVARQMPGK--VOVPLIHGQVYLANPGVIAIDAKTGDLIMEHROP--NIAT 123
DB 74 NLGLAWSYDESTRGVBATPLVDGVVYVSAPMSVVAIDAKTGKRLMTYDPOVPRDAY 133
QY 124 LNSGPEPTRGALVGTNVYFVSMNDHLVALDTATAGQVTFD----VDRGQEDWVSSSGP 179
DB 134 KGCCDVVNRGVALYQGVKVFAGAFDGRILVALDAATGKRVWEDPTLVDSKSYTI---TGAP 190

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OY 180 IVANG-VIYAGSTQYSPGCEVSGHDSATGEELMRYEIP-----RAGEEDETW 229
DB 191 RYVNGKVIINGGAEYGVNG-VITAYDAETGKQOMWYVYPPDPAEFENEMAAKAAV 249
OY 230 GNDYER-WMTG---AMQIYDPTNLVHYGSTAVGPASSETQSTPGG-TLYGTNRF 283
DB 250 --DPSGRYIINGGGGTVMYTMAFDPELNTMYIGTGACNGSKRLSPKGDNLVYASV-V 306
OY 284 AVRPDGEIVMRHQLPRNNDOCEFEEMVYN--VDVQPSYEMGLOSINRNATGER 341
DB 307 ALMPDGTGEIVMHIQETPGDNMTYTSODILLADLKIDGP-----RK 348
OY 342 VLTGVDPCKTGMQDAETGEELMARDTNYQNMISIDENG--ITYVNEDALIKELDEY 399
DB 349 VILHAP-KNGFEFVIDRTNGKFLSAKNFVDVWASGYDKNGRPVETPOADTSGKA- 403
OY 400 DYCPTFLGGRDMPSAALNDSGITFPLNNVCYDMAVDQESTMDVYNTSN----- 451
DB 404 DVPVGPFGAHNMHSMFHPKLGIAFLPAQHVP-LTADNKEW---VHNQKDSPEAHRGV 458
OY 452 -----VTKLPCKDMIGRIDAIDISTGRTLSVERAANSPVLSTGGVLFNGGTD 504
DB 459 GNNLGLVNAEPFRSKPEKRLTAMPDLQAKAVHRDHGPMWGTPLATAGNLVFGTADG 518
OY 505 YERALSQETGELTMOJRLATVASGOAISYENDGMQYALA-GGVSYSGLNSALAGERV 563
DB 519 RLVAVHAATGERTKMQAPGSSGVVAPVYLLDGRQYVSVAWVGQVYG-----LSQGS 572
OY 564 DSTAIGNAVYVAL 577
DB 573 DRQAPGR-VYTEVL 585

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RESULT 2
O46444 PRELIMINARY; PRT: 708 AA.
AC O46444
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, last annotation update)
DE OJUNHAEMOPROTEIN ETHANOL DEHYDROGENASE TYPE I PRECURSOR (EC 1.1.99.-)
(OH-EDH1).
GN QHEDH.
OS Comamonas testosteroni (Pseudomonas testosteroni).
OC Bacteria; Proteobacteria; beta subdivision; Comamonadaceae; Comamonas.
OX NCBI_TaxID=285;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 15667;
RX MEDLINE=96184549; PubMed=8654419;
RA Stoorvogel J., Kraayveld D.E., Van Sluis C.A., Jongejan J.A.,
De Vries S., Duine J.A.;
RT "Characterization of the gene encoding quinoxaline ethanol
dehydrogenase of Comamonas testosteroni.";
RL Eur. J. Biochem. 235:690-698(1996).
RN [2]
RP SEQUENCE OF 32-54 AND 477-490.
RC STRAIN=ATCC 15667;
RX MEDLINE=95324580; PubMed=7601151;
RA De Jong G.A.H., Geerlot A., Stoorvogel J., Jongejan J.A., De Vries S.,
Duine J.A.;
RT "Quinoxaline ethanol dehydrogenase from Comamonas testosteroni.
Purification, characterization, and reconstitution of the apoenzyme
with pyruvate and quinoxaline analogues.";
RL Eur. J. Biochem. 230:899-905(1996).
RP CHARACTERIZATION.
RX MEDLINE=86242113; PubMed=3521592;
RA Groen B.W., van Kleef M.A., Duine J.A.;
RT "Quinoxaline ethanol dehydrogenase apoenzyme from Pseudomonas
testosteroni.";
RL Biochem. J. 234:611-615(1986).

```

CC -1- FUNCTION: CATALYZES THE DYE-LINKED OXIDATION OF PRIMARY ALCOHOLS
CC TO THE CORRESPONDING ALDEHYDES AND THE (SUBSEQUENT) OXIDATION OF
CC THE ALDEHYDES TO CARBOXYLIC ACIDS.
CC -1- COFACTOR: POQ, HEME, AND CALCIUM.
CC -1- SUBUNIT: MONOMER.
CC -1- SUBCELLULAR LOCATION: PERIPLASMIC (POTENTIAL).
CC -1- INDUCTION: BY ETHANOL AND BUTANOL.
CC -1- SIMILARITY: TO ALCOHOL DEHYDROGENASE (ACCEPTOR) PROTEINS.
DR EMBL: X81880; CA57464.1; -.
DR HSSP: P38539; 4AAB.
DR InterPro: IPR001479; -.
DR InterPro: IPR002372; -.
DR InterPro: IPR003088; -.
DR Pfam: PF000034; cytochrome_c_1.
DR Pfam: PF01011; Bacterial_POQ_6.
DR PRINTS: PS00605; CYTCHROME_C1.
DR PROSITE: PS00363; BACTERIAL_POQ_1; 1.
DR PROSITE: PS00364; BACTERIAL_POQ_2; 1.
KW Signal; POQ; Heme; Calcium; Oxidoreductase; Periplasmic.
FT SIGNAL 1 31
FT CHAIN 32 708
FT TYPE 1.
FT BINDING 635 635 OJUNHAEMOPROTEIN ETHANOL DEHYDROGENASE
FT BINDING 638 638 HEME (COVALENT) (BY SIMILARITY).
FT METAL 639 639 HEME (COVALENT) (BY SIMILARITY).
FT METAL 639 639 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
SQ SEQUENCE 708 AA; 76822 MW; 99AB54BDD6ACB3 CRC64;

```

Query Match 18.9%; Score 583; DB 2; Length 708;
Best Local Similarity 27.9%; Pred. No. 6, 1e-33;
Matches 173; Conservative 95; Mismatches 271; Indels 82; Gaps 22;

```

OY 3 PTSLMASAGALALLAARPAQVTPVT-----DELANPP-AGEWISYQNGEN 50
DB 12 PGRVWMLLAACLG--SAAAFAPQTPGPAQAAAVQYVDGFEIRANARTDMPITGVDAE 69
OY 51 YRHSPLQITTEENVGOLVWARGMOPGK-VQYTPLIHGDVWVLANPQVIOAIDKTD 109
DB 70 TRSRDLQIYANAVKDLGLMSYNLESTRGEVTPVVDGIMVSSWSVHAIDRTN 129
OY 110 LIWEHRRLPNIATLNSFGP-PTRGALYGTNYFVSMNHLVALDTATG-----QVFPD 163
DB 130 RIWTFDQIDRSTGFGKCCDVVNRGVALMKGYVGAMPGRLIALDAKGEVHQNTFE 189
OY 164 VDGQGDMSNSGSPYVANGVYAGST-CQYSPGCEVSGHDSATGEELMRYEIP--- 219
DB 190 GQKGS-----LTTGAPRVEGKVIIGKRAEYGVRG-VITAYDAETGERKMWFSVPDP 244
OY 220 -----RAGEEDETWGNDEYEAHMTGA-----WQIYDPTNLVHYGSTAVGPASSETQ 268
DB 245 SKRFEDESKRAARTM--DPSGKMWELAGGGGTIMDSMTDAELNTMYVTGCGSPRSKRV 302
OY 269 RGTPTGTLGTNTRPAVRDPTGEIVMRHQLPRNNDOCEFEEMVYNVDVQSTEMGL 328
DB 303 RSPKGDNLVYLSIVALDPTGKYNHYQETPGDNMTYSTQPMILADIKI----- 353
OY 329 QSNPNPAATGERVVLGVPCCKTGMQDAETGEELMARDTNYQNMISIDENG-ITYVN 387
DB 354 -----AGKPRKVIILHAP-KNGFEFVIDRTNGKFLSAKNFVDVWASGYDKHGRPIG- 404
OY 388 EDALIKELDEYVCPYTFGLGGRDMPSAALNDSGITFPLNNVCYDMAVDQ-ETP----- 442
DB 405 --AAADGSKPQDAVGPFGALNNHMSNTPGTGLVYLPQAVNPVNLDDKKHFEHQAGP 462
OY 443 ---SMDVYNTSNVTKL-PGKDMIGRIDAIDISTGRTLSVERAANSPVLSTGGVVL 497
DB 463 GKQSGTGMNTAKFENABPPKSKPRGRLAMPVQAKAASVEHVSPPWNGTLLTAGNVV 522
OY 498 FNGGTIRYRALSQETGELTMOJRLATVASGOAISYENDGMQYALA-GGVSYSGLNS 556
DB 523 FQGTADGRLVAVHAATGERTKMQAPGSSGVVAPVYLLDGRQYVSVAWVGQVYG----- 577

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QY 557 ALGERVDSALGNAYVEAL 577
 DB 578 -LAARATEROGPG-TVTFV 596

RESULT 3

053362 PRELIMINARY; PRT; 742 AA.
 AC 053362; 044159;
 DT 01-NOV-1996 (Tremblrel. 01, Created)
 DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
 DT 01-OCT-2000 (Tremblrel. 15, Last annotation update)
 DE DEHYDROGENASE SUBUNIT OF ALCOHOL DEHYDROGENASE.
 OS Acetobacter pasteurianus.
 OC Bacteria; Proteobacteria; alpha subdivision; Acetobacteraceae;
 OC Acetobacter.
 OX NCBI_TaxID=438;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-NC11380;
 RX MEDLINE=94042848; PubMed=8226628;
 RA Takemura H., Kondo K., Horinouchi S., Beppu T.;
 RT "Induction by ethanol of alcohol dehydrogenase activity in Acetobacter
 pasteurianus."
 RL J. Bacteriol. 175:6857-6866(1993).
 DR EMBL: D13893; BAA40252.1; -
 DR HSSP; P38539; 4A4H
 DR InterPro; IPR001479; -
 DR InterPro; IPR002372; -
 DR Pfam; PF01011; Bacterial_P00; 6.
 DR PROSITE; PS00363; BACTERIAL_P00_1; 1.
 DR PROSITE; PS00364; BACTERIAL_P00_2; 1.
 SQ SEQUENCE 742 AA; 81680 MW; 031C4E9B6B13EC98 CRC64;

Query Match 18.2%; Score 561; DB 2; Length 742;
 Best Local Similarity 28.5%; Pred. No. 2.4e-31;
 Matches 173; Conservative 90; Mismatches 248; Indels 96; Gaps 21;

QY 11 AALALLAFAAQTPTVDL--ANPPAGWISYGOENYRHSPLQITTEVNGOLO 68
 DB 23 AALPFAAFAADGNGTGEAIIHADHPENWLSYGRYSQRTSPIDQIRSNVGLK 82
 QY 69 LVMARGMOGKVO-VTPILHDGVMILANPGDYLQAIIDAKTGDLWEHRRLP-NIATLNS 126
 DB 83 LAMVYTLIDNRQGEATPLVDSIMATITNWSKMEALDAATGKLMQYPRKVGNIADGCG 142
 QY 127 FGEPTRGMALYGTNVYFVSMNDHLVALDTANGVTFD-----DRGGEEDMYSNNSGPI- 180
 DB 143 CDTVNRGAGYNGKVFMCFTDGRILVAADAKTGKWEVETIPADASLGKORSYTVDGAVR 202
 QY 181 VANGVIVAGSTOQYSPFGC-FVSGHDSATGEELMRNYFIKPRAGEG----- 226
 DB 203 VAKGLVLIGN--GGSEFGARFVSAPDAETGKLMKRYTVPNKKPEPHAVADVNLMSKA 260
 QY 227 -ETWGDYDARMT-----GANGQITPDYPTNLVHGSTAVPASERGTGPGTLY-- 277
 DB 261 YKTWGP--KGAVRGGGGTVDLSLYDPDLYL--LAVG-----NGSPWNKKYKSE 309
 QY 278 ---GTN---TRAVRDTGEIWMHQTLPKDNWDOCTFEEMAVTVNVOPSTEMEGLQSI 331
 DB 310 GIGSNLFLGSIVALKRETEGEYVWHFOATPMDQMDYTSVOQIMTLMPV----- 357
 QY 332 NPPAAGE--RYLTGVPCCTGTMQGFDAETGEFLMARODNYQNMIESIDE-NGITVND 389
 DB 358 ---NGEKRHYIWAAP-KNGEFTYLDATKTEGLAGKKNVYQNMANGDLPLTGRITLYND 411
 QY 390 AILKEIDVEDYVCPFLGGRDWPSSALNDPSGIYPLINVCY-----DMKA 436
 DB 412 GLTTLTGKFWYGIPLGLAHNFEMGAYSPKTHLYLPAHQIFPGYKNGVGGKPPHDAWN 471
 QY 437 VDOEFTSMQVYNTSNVTKLPKGDIMIGRIDALDIDISIGRTLSVERAANYSVLSTGGCV 496

DB 472 VGLDMTKNGLPDTP-ARTAYIKDLHGMLIANDPVKMETVWKIDHKGPWNGVYLATGDL 530
 QY 497 LFNGGTRDYFRALSOETGETIMQTRLATVAGGQATSEYDGMQYVA-----IAGG 546
 DB 531 LFGGLANGEEHAYDATNGSULYKFDASGILASPMYTVNGKQYVAVEVGMGIYPIISMG 590
 QY 547 GVSYSGG 553
 DB 591 GVGRTSG 597

RESULT 4

09EYW8 PRELIMINARY; PRT; 601 AA.
 AC 09EYW8;
 DT 01-MAR-2001 (Tremblrel. 16, Created)
 DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
 DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
 DE METHANOL DEHYDROGENASE LARGE SUBUNIT-LIKE PROTEIN.
 GN MxA.
 OS Rhizobium meliloti (Sinorhizobium meliloti).
 OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
 OC Rhizobiaceae; Sinorhizobium.
 OX NCBI_TaxID=382;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-RM1021;
 RA Penner B.J., Tiwari R.P., Dillworth M.J.;
 RT "Regulation of Cl assimilation in Sinorhizobium meliloti";
 RL Submitted (SEP-2000) to the EMBL/Genbank/DBJ databases.
 DR EMBL: AF309488; A631643.1; -
 SQ SEQUENCE 601 AA; 65686 MW; 09F743726B2E2A83 CRC64;

Query Match 18.1%; Score 560; DB 2; Length 601;
 Best Local Similarity 27.1%; Pred. No. 2e-31;
 Matches 171; Conservative 109; Mismatches 248; Indels 104; Gaps 24;

QY 14 LALLAFAFAAQTPTVDL--LANPPAGWISYGOENYRHSPLQITTEVNGOLO 71
 DB 8 LAIMSIGGAAVAFANDELQKLIIDP-NQWALITGDVYANLRYSLQIDINKDNGKLIQVAV 66
 QY 72 --ANGMOGKVOYTPILHDGVMILANPGDYLQAIIDAKTGDLWEHRRLP-NIATLNS 126
 DB 67 TFSYGVLRGH-EGSPILVIGDLMVYTPFPMTVYALDSKSGQLYWKYEPKODPVVIVMC 125
 QY 127 FGEPTRGMALYGTNVYFVSMNDHLVALDTANGVTFD-----DRGGEEDMYSNNSGPI-VANGV 185
 DB 126 CDTVNRGAGYNAADNKIFLHQADTYVVALDARTGKTYWSYKNGDARTGNTATATVPVADKI 185
 QY 186 IVAGSTOQYSPFGCFVSGHDSATGEELMRNYFI-----PRAGEGDE 227
 DB 186 LVGISGGEFVGRG-HVTAYSMADGKVLMRGYSMPDSDTLIDPEKTHLKGPKGKDSGLT 244
 QY 228 TWGNDYDARMTG---AMGQITPDYPTNLVHGSTAVPASERGTGPGTLYGNTNRA 284
 DB 245 TWESD---QWITGGGTWGTWGYSDPEENLYYGTGNSTWMPYOR--PGDNRW-SMTIFA 296
 QY 285 VRPDGEIWMHQTLPKDNWDOCTFEEMAVTVNVOPSTEMEGLQSIINPPAAGEERVLT 344
 DB 299 RDVDTGAKKWLYQMTPHDEMVDYGVNEKILTGQIHDK-----DRKILT 342
 QY 345 GVPCKTGTMQGFDAETGEFL-----WARTNYQNMIE-----SIDNGI 383
 DB 343 HFD-RNGFTYMDRVTGELLVAEKYDPTVWNAETEVVMDPKSDKGRPOVYAOYSTEOG- 400
 QY 384 VTVMEDALIKELDEYDVCPTFLGGRDWPSSALNDPSGIYFIPINNYCYDMAVDOEFTS 443
 DB 401 ---EDNTT-----GCPALGTGKDOQPRAYSPTKLELTVPNHNCMDYEPFRYSYA 450
 QY 444 MDVYNTSNVTKLPKGDIMIGRIDALDIDISIGRTLSVERAANYSVLSTGGCVLNG 500
 DB 451 GQPIYVATLSMYP-KDSHGGMGNFIACDNKEKIKMSLPEFFVSMGALATADVYFYG 509

QY 501 GTDPRFALSOETETLMTOTRLATVASGOAISYEDVMQVATAGS-----GVSYGSLN 555
DB 510 TLBGYLAKVADATKATKELRYKTPSGVIGNMVYARBGKQYVAVLSGVGMAGIGLAAGLT 569
QY 556 SALAG-----ERVDSIAIGNAVYVFPALPO 579
DB 570 NPTEGLAVGVGSDLSNMYNALGGTLEFKLPE 601

RESULT 5
Q9P9U2 PRELIMINARY: PRT: 695 AA.
ID Q9P9U2; 09F902;
AC Q9F902;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE ALCOHOL DEHYDROGENASE.
GN ADH.
OS Pseudomonas stutzeri (Pseudomonas perfectomarina).
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Pseudomonas.
OX NCBI_TaxID=316;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BC-2;
RA Chang C.-H., Herrick J.B., Okinaka R.T., Brainard J.B.,
RA Terrylliger T.C.;
RT "Identification and characterization of genes activated by 2-
RT chloroethanol in Pseudomonas stutzeri BC-2."
RT Submitted (AUG-1999) to the EMBL/Genbank/DBJ databases.
DR EMBL: AF176640; AAG09249.1;
DR Ffam: AF176640; AAG09249.1;
SQ SEQUENCE 695 AA: 75842 MW; D29A698A642E1A83 CRC64;

Query Match 17.8%; Score 549.5; DB 2; Length 695;
Best Local Similarity 29.28; Pred. No. 1.4e-30;
Matches 168; Conservative 89; Mismatches 259; Indels 59; Gaps 21;

QY 15 ALLAAFAFAQVPTVDEL--ANPAGIEWISYGOQENVRHSPFLQITTEVNGOLVMA 72
DB 16 ALLVA-AGQAQAKVDEAARASEQDSERLSHGRTYAEORSPLQIDAGNVGKIGLAWY 74
QY 73 KGMQGRK-VQVTPLIHDGVMIYLANGVYIAQIDARTGDLIWEHRQD-NIATLNSFGE 130
DB 75 LDLENNRGLEATPLVSDGVYASLSMSRYMAVDLSGKRLMQFDQVDRGHSRYCCDAV 134
QY 131 TFGMALXGNNYFVSWDNLVADLTATGQVTPVDVROGEDMVSNSCPITYANG-VIYAG 189
DB 135 NGGVALLMGKTVYVGLDRLIALDAKTRELSQETTPDAPKPSITGAPRVKGVITGN 194
QY 190 STQYSPFGCFVSHDSATGEELMRYNFIPIRAGE-----EGDET-VGNDYEARW 237
DB 195 GGAEGVGVG-FPSATDAETGKAMRFYTP--GDPAPYEHPELAEAKTKKQDY--W 248
QY 238 MTG-----AMGOITYPVNLVHGSTAVGPASETQRTGGTLYGTNTRFAVRPDTGEIV 293
DB 249 KLGGGGVWDMADYPELDLYIGTGNGSPNNREIRSPGDNLYLSIALRPDSKRL 308
QY 294 WRHOFLEPDMNDQECTFEMMTNVDPVQSTMEGQASINPMAAIGERVLVGVCKGTGM 353
DB 309 WHYQTTPEETWDFATQOITLATL-----BLDG-----KPRVLMQAP-KNGFF 351
QY 354 WQFPAETGEFLMARDTNQNMIESID-ENGIVVNEDAILKELDEVEDVCPTEFLGRDM 411
DB 352 YVLDRAETGELLISAEKFGVTAKEKVDLATGRPEVPGSRYKKEQVMM--PSSFGAHNM 408
QY 412 PSALINPDSGYTFPLPLNNVCYDMAVDOEFTSMQVNT---SNVTKLPSPKDM-GRID 466
DB 409 HSMSPNPQTLMIYIPYORIPGVYRNEGATFKIDGLNTGTGFSPTHEIP--RDVAGSALL 466
QY 467 AIDISTGTLMSVERAANYSPLVSTGGGVLFNGSTDRYFALSOETETLMTOTRLATVA 526

DB 467 AMDPVROEAMRVHPSFYNGGTLSTAGNLVFGGTADGQLHAYSADKQRLMSFAQTGI 526
QY 527 SGOAISYEDVMQVATAGS-----GVSYGSLNSALA 559
DB 527 VAAPISFSLDGEYVAVVAGGGAAPLIGDPAALA 561

RESULT 6
P71509 PRELIMINARY: PRT: 601 AA.
ID P71509;
AC P71509;
DT 01-FEB-1997 (TREMBLrel. 02, Created)
DT 01-FEB-1997 (TREMBLrel. 02, Last sequence update)
DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
DE METHANOL DEHYDROGENASE LARGE SUBUNIT HOMOLOG.
GN MXP.
OS Methylobacterium extorquens.
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Methylobacterium group; Methylobacterium.
OX NCBI_TaxID=408;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AMI;
RX MEDLINE=97312011; Pubmed=9168622;
RA Chistoserdova L., Lidstrom M.E.;
RT "Molecular and mutational analysis of a DNA region separating two
RT methyloctrophy gene clusters in Methylobacterium extorquens AM1."
RL Microbiology 143:0-0(0).
DR EMBL: U72662; AAB58890.1;
DR HSSP: P38539; 4AAB.
DR InterPro: IPR002372;
DR Pfam: PF01011; Bacterial_PQQ; 7.
SQ SEQUENCE 601 AA: 64952 MW; 68FA5C7059CBB239 CRC64;

Query Match 17.4%; Score 537.5; DB 2; Length 601;
Best Local Similarity 26.4%; Pred. No. 7.8e-30;
Matches 166; Conservative 115; Mismatches 267; Indels 81; Gaps 23;

QY 1 MKPISLMAAGALALLAFAFAQVPTVDELANPPAGIEWISYGOQENVRHSPFLQIT 60
DB 1 MRAVHLLALAGLAA--ASPALANESYLKG--VAP--ABQVLOTVYANTRYSKLDQIN 54
QY 61 TENYGOLOLV--ARGMQPKQVQVTPLIHDGVMIYLANP--GDVIOQIDARTG--DLIWEHR- 115
DB 55 ASANKNLQVAMTSTGLRHH--EGSPLYVGNINMIVHTPPNIIYALDLOGAKIVKYPE 113
QY 116 RQLEPNATLNSFGEPTFGMALYGTNMYFVSWDNLVADLTATGQVTPVDVROGEDMVS 175
DB 114 KQDSVIVPVCCTVNRGLAYADGAILLHQADTTLVSLDAKSGKVMYSKNGDPSKGETN 173
QY 176 SSGGVYANGVYVAGSTQYSPFGCFVSHDSATGEELMRYNFIPIRAGE----- 218
DB 174 TATVLPVKRVYIVGISGEGGVCHVATYADLKGSKGWRGYSIGPDDQILVPEKTSLSG 233
QY 219 -PRAGEGDETTGNDYEARWMTG---AMGOITYPVNLVHGSTAVGPASETQRTGGT 274
DB 234 KPLAKDSLSLKTWBGD---QMKTGCGCTGWFSTDPRLDLMTYGS--NSTGNPKORPBD 288
QY 275 TLVGTNTRFAVRPDTGEIYWRHOFLEPDMNDQECTFEMMTNVDPVQSTMEGQASIN 334
DB 289 NKW-SMTIMARNDDTGMKAVVYQMPHDEWDPDGINEMILTD-----QKFDG----- 334
QY 335 AANGERVVLGVCKGTGMQFPAETGEFLMARDTN-QNMIESID-ENGIVVNEDAIL 392
DB 335 ---KDRPLTHPD-RNGFGTTLDRATGEVLAKEFDPVVMATKYVLDLKGSTYGRPLV 390
QY 393 KELDEYD-----VCPTEFLGRDMPAALNPDGSIYFPLNNVCYDMAVDOEFTSM 444
DB 391 SKSTEDNGDVMSKICRAALGTCKQDPAAPSPKGLGYVPTNHYCMYDEFPRTYITG 450
QY 445 DVYNTSVTKLP-PGR-DMIGRIDALISTGTLMSVERAANYSPLVSTGGGVLFNGST 502

Db 451 QPYGATLMTVPAPSHGMCNFIAMDNLOCKIKWNPEDQFSAGALATSGDLYFYCTL 510
 QY 503 DRYFRALSGEETLMQTRLATVASGOAISTEVDMQYVALAG-----GVSYSGSLNSA 557
 Db 511 EGFIAKAVDSKTKELKFKPPSGIIGNMYIEHKQHVAVLSGVGMAGIGLAAGLTP 570
 QY 558 LAG-----ERVDSIAIGNAVYFALP 578
 Db 571 NAGLGAVGAYALSSYTNLGGQLVYFSLP 599

RESULT 7

024759 PRELIMINARY; PRT; 633 AA.
 ID 024759
 AC 024759
 DT 01-JAN-1998 (TREMBlrel. 05, Created)
 DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
 DT 01-JUN-2000 (TREMBlrel. 14, Last annotation update)
 DE METHANOL DEHYDROGENASE ALPHA UNIT PRECURSOR (EC 1.1.99.8).
 GN Mxap.
 OS Hyphomicrobium methylovorum.
 OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
 OC Hyphomicrobium group; Hyphomicrobium.
 OX NCBI_TaxID=84;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=GM2;
 RX MEDLINE=97457202; PubMed=9311140;
 RA Tanaka Y., Yoshida T., Watanabe K., Izumi Y., Mitsunaga T.;
 RT "Cloning and analysis of methanol oxidation genes in the methylovoroph
 RT Hyphomicrobium methylovorum GM2";
 RL FEMS Microbiol. Lett. 154:397-401(1997).
 DR EMBL: AB004097; BAA3272.1;
 DR HSSP: P38539; 4AAH.
 DR InterPro: IPR001479;
 DR InterPro: IPR002372;
 DR Pfam: PF01011; Bacterial_POQ_7.
 DR PROSITE: PS00363; BACTERIAL_POQ_1;
 DR PROSITE: PS00364; BACTERIAL_POQ_2;
 KW Signal; Oxidoreductase.
 FT SIGNAL 1 34 POTENTIAL.
 FT CHAIN 35 633 POTENTIAL.
 SO SEQUENCE 633 AA; 69852 MW; BA7A23A2779E2C1B CRC64;

Query Match 15.5%; Score 479.5; DB 2; Length 633;
 Best Local Similarity 25.0%; Pred. No. 1e-25;
 Matches 158; Conservative 116; Mismatches 270; Indels 87; Gaps 22;

QY 6 LMASGALALAAPAFQVPTVDELLANPAGE-WISYGNONBYRHSPLTQITTEV 64
 Db 12 LMSASGALALAAVLOVAVSSAVANDKLELSKSNENWVPGKNYSNNYSESTQVNAENV 71
 QY 65 GOLQVWARGMOPKGV---QVTPPLIHIDGVYMLAN--PGDVIQAIIDAKTGDLIWEHR-RQL 118
 Db 72 KQKRWMS--FSTGELHGEAPLVIGDMYVHSSFPNKFALINDSGHILMOHSPKQD 129
 QY 119 PNATITNSGEPTRGMALYGTN-----YFVSMNHIALDTATGQVTFEDVDRGGEDM 172
 Db 130 PAARSVACCDLVNRLGLAYVPGDKTPALVITKQLDGHVALNAKGELEFWEKVENGDIKYG 189
 QY 173 VNSNSGPITVANGVYAGTCQYSPFCFVSGHDSATGEELMRYFI----- 218
 Db 190 QLTITQAPYVYHDLAIYVSSGALGVNGHYTAVNVKTGDEQAMRYVATGPEDEIGLADDFNS 249
 QY 219 --PRAGEE--GDETWGNDYEARMTGA---WGQITYPVTVNLVHGSTAVGASERQRT 271
 Db 250 ANHYQKQKIGTATWEGD---AWKIGGTTNMGWYAYDPQANLIYVSGNPAPWNETMR-- 304
 QY 272 PGITIGTNRFAVRPDGTGFIWRHQTLPNDNMDCETFEEMVTVNDVOSTEMEGLOSI 331
 Db 305 PGDNKM-TMTITRADADTGKMKFGYOKTTHDEMDFAGVAVIMLSE-----QIDKE----- 353

QY 332 NPNAATGERRVLTGVCCKTGMQPDATGEELMA--RDTNYKNMIESIDENGIVTNE 388
 Db 354 -----GKKRKLTHDRNGIYVTLIDRENGDLISADKLDDT--VNVFKHVDLKSGLPARD 405
 QY 389 DALKELDVE-YVOCPTFLGGRDWPASALNPDSGVIFPLNNVCYDMAVVDDEFTSMUY 447
 Db 406 PEFGRTRDHKGTETICPSANGYHNOGHDSYDPKQLEFFKGINHCADMEFFMLPYRAGQFF 465
 QY 448 NTSNVTKLP-PGKDM-----IGRIDAIDISTGRTLSVERAANYSPVLSTGGVLFNGG 501
 Db 466 VGATIMMYEPKGRDQNYLGLGQIKAVNATITNYKKEHHERBSVMGGLATAGNLVYGT 525
 QY 502 TDYFRALSGEETLMQTRLATVASGOAISTEVDMQYVALAG-----GVSYSGSLNS 556
 Db 526 LDGFLKARNSDDTGELLMKHKLPSGVIGVYPMYIEHKQVQYIAVMSGVGMGVLVFDLQD 585
 QY 557 ALAG-----ERVDSIAIGNAVYFALP 577
 Db 586 PTAGLGAVGAFKMLQRY--TOMGGSLEVFSL 614

RESULT 8

09L935 PRELIMINARY; PRT; 599 AA.
 ID 09L935
 AC 09L935
 DT 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
 DE METHANOL DEHYDROGENASE LARGE SUBUNIT.
 GN Mxap.
 OS Methylovorus sp. (strain SSL / DSM 11726).
 OC Bacteria; Proteobacteria; beta subdivision; Methylophilus group;
 OC Methylovorus.
 OX NCBI_TaxID=81683;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SSL;
 RA Kim Y.M.;
 RT "Cloning and nucleotide sequence of mxap gene of Methylovorus sp.
 RT strain SSL DSM11726";
 RL Submitted (SEP-1999) to the EMBL/Genbank/DBJ databases.
 DR EMBL: AF184915; AAD56237.2;
 DR InterPro: IPR001479;
 DR InterPro: IPR002372;
 DR Pfam: PF01011; Bacterial_POQ_7.
 DR PROSITE: PS00364; BACTERIAL_POQ_2;
 SO SEQUENCE 599 AA; 65133 MW; DB6F4B5D871BC91 CRC64;

Query Match 15.3%; Score 473; DB 2; Length 599;
 Best Local Similarity 25.2%; Pred. No. 2.8e-25;
 Matches 157; Conservative 108; Mismatches 281; Indels 76; Gaps 21;

QY 4 TSLMASGALALAAPAFQVPTVDELLANPAGE-WISYGNONBYRHSPLTQITTEV 63
 Db 6 TATGFAVAGLALSMBSVLAADSLLEALGNP--NMWMTQGTGYTOHRSLSQITGN 63
 QY 64 VGOLQV---VWARGMOPKGVQVTPPLIHIDGVYMLAN--PGDVIQAIIDAKTGDLIWEHR-RQ 117
 Db 64 VKNLESGLGHSTGLIGH-EGAPLVIGDMYITWPPNNTFALNLAEDEKIVQHRPKQ 122
 QY 118 LPNATITNSGEPTRGMALYGTN---YFVSMNHIALDTATGQVTFEDVDRGGEDMVSNS 177
 Db 123 DASVKAIVACCDIVNRLGLAYDDGHIFKTQLDHLVASDAKTKELMKMKNCDPAVGSTITQ 182
 QY 178 GPIVANGVIVAGTCQYSPFCFVSGHDSATGEELMRYFI-----P 219
 Db 183 APFAVKGAVLVG--CSGELGVNGVYVTAIDOKTELVWRSAVATGPDELNLAKDFNKNP 240
 QY 220 RAGEE--GDETWGNDYEARMTGA---WGQITYPVTVNLVHGSTAVGASERQRT 274
 Db 241 HYQWGLGTKTWEGE---GMRIGGTTNMGWYAYDPKLNLFYVSGNPAPWNETMR--PGD 295

QY 275 TLVGTNREAVRPDTEGEIYWRHQTLPDRNDMDQCFEMAVTVNDVOPSTMEGLSINP 334
 Db 296 NKV-TWTIMARVDYDGAAGWYOKTPHDEMDPAGVNMILLTOAVNGKIO----- 344
 QY 335 AATGERRVLTGVCKTGTMMQDAETGEFLMARDTN-YONMTESIDENCIIVTNEDALIK 393
 Db 345 -----PLTLTHVD-RNGIYITLNRQTSIVQAKAYDPANVKKYDLKGLVDRPEFEST 397
 QY 394 ELDFVE-YDVCPTFLGGRDPSAALNDPDSGIYFLPLNNVCYDMAADQETSMDEVNTSNV 452
 Db 398 RMDHKNTNCPSAMGPHNGLDAYDPDSTRTFYFGLNHTICMDPEPMLPRAGQFVGATL 457
 QY 453 TKLP-----PKDMIGRIDAIDISTGTRLMSVERAANSPVLTSGGVLFNGTDRYERA 508
 Db 458 AMYPGNPGPTKKEMGOVLAMDGVTEGKWTKEKFSVWGTLATGGLVFTYTLGDNKKA 517
 QY 509 LSGEGETLMQTRLATVASGQAISEVDGMQVAI---AGG--GVSYSGLSALAG--- 560
 Db 518 LKTNKKEITWKEKMPGSAIGAPMSYAKGKOYIATNYGVGMPGVGLVFDLTPSAGLGA 577
 QY 561 -----ERVDSIAIGNAVYFEAL 577
 Db 578 VGAFKELQNTQMGGVWFGL 599

RESULT 9
 059540 PRELIMINARY: PRT: 573 AA.
 AC 059540:
 DT 01-NOV-1996 (Tremblrel. 01, Created)
 DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
 DT 01-MAY-2000 (Tremblrel. 13, Last annotation update)
 DE METHANOL DEHYDROGENASE HEAVY SUBUNIT (EC 1.1.99.8) (ALCOHOL
 DE DEHYDROGENASE (ACCEPTOR)).
 OS Methylophilus methylotrophus (Bacterium M3A1).
 OC Bacteria; Proteobacteria; beta subdivision; Methylophilus group;
 CC Methylophilus.
 OK NCBI_TaxID=17;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=M3A1;
 RA Xia Z. X., Dai W. W., Zhang Y. F., He Y. N., White S. A., Boyd G. D.,
 RA Matthews F. S.,
 RL Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.
 CC -I- CATALYTIC ACTIVITY: A PRIMARY ALCOHOL + ACCEPTOR = AN ALDEHYDE +
 -I- REDUCED ACCEPTOR.
 CC -I- COFACTOR: POO.
 DR EMBL: U41040: AAA83765.1; -.
 DR HSSP: P38539; 4NAH.
 DR InterPro: IPR001479; -.
 DR InterPro: IPR002372; -.
 DR Pfam: PF01011; Bacterial_POO; 7.
 DR PROSITE: PS00364; BACTERIAL_POO_2; 1.
 KW Oxidoreductase.
 SQ SEQUENCE 573 AA; 62635 MW; A06C9B3091BB8F0C CRC64;

Query Match 14.2%; Score 439.5; DB 2; Length 573;
 Best Local Similarity 24.5%; Pred. No. 6e-23;
 Matches 146; Conservative 99; Mismatches 259; Indels 93; Gaps 21;
 QY 38 AGEMISYQGNQENYRHSPLQITTEYNGQLQLYW--ARGMQPGKVQVTPLIHGVML-- 93
 Db 13 AGAPRIATGYYGSOHNSPLQINSKNVKAAMSFSTGLNCH-BGAPLVIDMMYVHS 71
 QY 94 ANPGDVQALDAKTDGLIWEHR-RQLEPNITLNSFGEPTFGMALYGTNTYFVSWDNLVA 152
 Db 72 AFENNYTALNLDNPGKIVMWHKPKODASTKAVCCDVVDRLGAYGAGQIYKKQANGHLLA 131
 QY 153 LDTATGVTFDVDRGQGEDMWSNGPIVANGVIAGSTQYSPFG--FVSGHDSATGE 210
 Db 132 LDKATGIMNEVEYCDPKVGSSTLTQAPFVAKDTVLKG--CSGAEIVRGAVNAFDLKTGE 189

QY 211 ELWR-----NYFIPRAGE--EGDETNGNDYEAMWTGA---WQIITYDP 249
 Db 190 LKWRAPATGSDSDSVRLAKDFNSANPHYGOFGLTGKTEGD---AMKIGGGINNGWYAYDP 246
 QY 250 VTNLVHYGSTAVGASSETQSTQGTGPG-----TLVGTNREAVRPDTEGEIYWRHQTLPDRNW 304
 Db 247 KLNLFYSSGNAPAWNENMR--PGDNKWTMTIWRDL-----DTGAANKGYOKTPIDEN 298
 QY 305 DQCFEMAVTVNDVOPSTMEGLSINPNAANGERRVLTGVCKTGTMMQDAETGEFL 364
 Db 299 DFAGVNMVLTLD-----QPVN-----GKMTPLSHIDRNLITLTLRENGNLI 341
 QY 365 WARDTN-YONMTESIDENGIIVTNEDALIKEIDVE-YDVCPTFLGGRDPSAALNDPDSGI 422
 Db 342 VAERVDAVNVFKVVDLKTGTPVDRPEFATRMQKNTNCPSAMGPHNGVDSDPSRT 401
 QY 423 YFPLNNVCYDMAADQETSMDEVNTSNVTKLP---PKDMIGRIDAIDISTGTRLMS 478
 Db 402 LYAGLNHCMDWEPMLPYRAGQFVGATLAMYPGNPGPTKKEMGOIRAFDLTTGKAKWT 461
 QY 479 VERAANYSPLVLTSGGVLFNGTDRIFRALSOETGETLMQTRLATVASGQAISEVDGM 538
 Db 462 KWEKFAAMGGTLTYTKGGLVYATLDGLKALDNKDKGELNMFPMPSGIGSPMTYFSGK 521
 QY 539 QYVAIAGGVSYSGS-----LNSALAG-----ERVDSIAIGNAVYFEAL 577
 Db 522 QYI-----GSMTYGVGMPGVGLVFDLTPSAGLGAIVGAFRELQNTQMGGVWFGL 573

RESULT 10
 09X2S5 PRELIMINARY: PRT: 790 AA.
 ID 09X2S5:
 AC 09X2S5:
 DT 01-NOV-1999 (Tremblrel. 12, Created)
 DT 01-NOV-1999 (Tremblrel. 12, Last sequence update)
 DT 01-MAY-2000 (Tremblrel. 13, Last annotation update)
 DE GLUCOSE DEHYDROGENASE.
 GN GDH.
 OS Pantoea citrea.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Pantoea.
 OK NCBI_TaxID=53336;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=1056R;
 RX MEDLINE=99303331; PubMed=10376838;
 RA Fujol C. J., Kado C. I.;
 RT "gdhB, a gene encoding a second quinoprotein glucose dehydrogenase in
 RT Pantoea citrea, is required for pink disease of pineapple."
 RL Microbiology 145:1217-1226(1999).
 DR EMBL: AF050503; A023735.1; -.
 DR InterPro: IPR001479; -.
 DR InterPro: IPR002372; -.
 DR Pfam: PF01011; Bacterial_POO; 7.
 DR PROSITE: PS00364; BACTERIAL_POO_2; 1.
 SQ SEQUENCE 790 AA; 85681 MW; 88BB7625E0A5F089 CRC64;

Query Match 11.8%; Score 365.5; DB 2; Length 790;
 Best Local Similarity 23.9%; Pred. No. 1.6e-17;
 Matches 169; Conservative 78; Mismatches 238; Indels 221; Gaps 34;
 QY 27 PYTDLAPPPAGEMISYQGNQENYRHSPLQITTEYNGQLQLYW-----RGMOPK 79
 Db 152 PATOPVSAGK---DWTAVCGTQAGDRYSSLQINSNVKNLQVAVTQSGDVKKRPDDGE 208
 QY 80 V--QVTPLTLDGVDVLANGVDTQALDAKTDGLIWEHRQLEPNITLNSFGEPT-RGVAL 136
 Db 209 ITNESPIPLAKGNLTYTGAHQILVALIDATGKEKN--RFPDKIYDPTFGHMTQGVSY 265
 QY 137 YGTN-----VFEVSWDNLVALDTATGATGVTPVDVRGQGEDM----- 172
 Db 266 HDFNTATDPQAPVSPACSRRIYLPVNDGRILAVDAENGQLCKDFGNNGELDLQHQDPN 325

QY 173 ---VSNSSGPVIANGVIV-AGS-TCQYS---PFGCFVSGHSDATGEELMRNFTRAG 222
Db 326 AFGPGYEFTSPVITDVKVIVAGAVTNTSTREPSG-VINGFDVTKKLMA--FDGAK 382
QY 223 E-----EGDETWNDXEARMWTGAMCOITVDPTNLNVHGSTAVGSPASFTQSTPGTIL 276
Db 383 DPNAIIPADGCHCSANS-----PNSMAPAAVDPKLDLVLYLPMGVTPFDIMCGNRTPEEH 436
QY 277 YGINTRAVAREDTGELIYWRHOTLPRDWMDOCTEEMAVTNAVDPSTEMEGLOSINPAA 336
Db 437 YASGI-LALNATTKCKEMFQYVTHHDLMDM-----IPAPS-----LADITDK-- 479
QY 337 TGEERVLTVGVCCKTGMWQFAETGEF----- 363
Db 480 DGNKVPVYVYPTKGNIFVLNRATGQLVPRAREAVQGAAGKQHTSATQPFELTRPE 539
QY 364 -----LWADNTYQNNI-----ESIDENGIVT-VNEDAILKELDYDYDVCPPFLGGRD 410
Db 540 AKLTDSKMWG-GTMFDMQICRIMFKRLHYNGTFPPSBQGL-----VEPNLGMFE 590
QY 411 WPSALNPDSGITYPLPLNNVCYDMAVDOETSDMYNTSVTKLPEGKMDIGR----- 464
Db 591 WGGISLVN--SSSEFALIN-----PMQLPVYSKILIPGRN-NMMEGKNAGSGSGGEGAG 640
QY 465 -----IDAIDISTGRTLSVEEAAANYS----- 487
Db 641 LQHNMYVPFVELNPFSLPGLPCMEPSWGFVSANIKTNDIWMKKRIGTRIDSGGPILP 700
QY 488 -PV-----LSTGGVLFNGGT-DRYPRALSOETGETLIMOTRIATVASGA--ISY 533
Db 701 PPIYVGTPLMGAPITTAGNIFFIATLDDYIRAVSVRGKLLMQARLP--AGCATPATY 758
QY 534 EVDGMOY-VAIAGGCVSTGSGLSNALSAGERVDSRIGANVYVFLP 578
Db 759 EVDGKQYLVIVAGGHSFG-----TKMGYIIAYKLIP 790

RESULT 11
Q91115 PRELIMINARY: PRT: 803 AA.
AC Q91115
DT 01-MAR-2001 (TREMblrel, 16, Created)
DT 01-MAR-2001 (TREMblrel, 16, Last sequence update)
DT 01-MAR-2001 (TREMblrel, 16, Last annotation update)
DE GLUCOSE DEHYDROGENASE.
GN GCD OR PA2290.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; gamma subphylum; Pseudomonadaceae;
OC Pseudomonas.
DX NCBI_TaxID=287;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-PA01;
RX MEDLINE=20437337; PubMed=10984043;
RA Hickey C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warren P.,
RA Rader R.L., Goltzy L., Tolentino E., Westbrock-Wadman S., Yuan Y.,
RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Lardig K., Lim R.M.,
RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
RA Reizer J., Sater M.H., Hancock R.E.W., Lory S., Olson M.V.;
RT "Complete genome sequence of Pseudomonas aeruginosa PA01, an
RT opportunistic pathogen.";
RL Nature 406:959-964(2000).
DR EMBL, AE004654; AAC05678.1; -
DR InterPro: IPR002372; -
DR Pfam: PF01011; Bacterial_PQO; 7.
SQ SEQUENCE 803 AA; 86217 MW; 7DDF46B0FE5ED249 CRC64;

Query Match	10.6%;	Score 327;	DB 2;	length 803;
Best Local Similarity	21.9%;	Pred. No. 8.7e-15;		
Matches 166;	Conservative 84;	Mismatches 265;	Indels 244;	Gaps 32;

OY	6	LIM-----ASGALALLAAFAQVPTVDELLANP-----	36
Db	103	LIMLPFRPELLADGPARPLGTALCVAVVLGAAGAAVGSG--FTNGQIVIGRIDRDSGMTST	161
OY	37	----PAGEWISTVCQONENYRHSPILQITTEENVGOLUWMARGMOPGRK-----	81
Db	162	APAMPDDMWATYRTETFGDRISPELQKITPANVGQLEEMNR---ITGDLLPRADDELLETNE	219
OY	82	VTEPLIHGGVVLANPDGVLOIALDKTGLIWEHRRLDNPNIATLSFGEPT- RGMALYGTN	140
Db	220	NTEPLAKVMGLIACTAHSKYLIALDPDTGAITRFDPQIQSPVGFKFAHMCRCGVSYDEE	279
OY	141	VY-----EVSNNHLVALDFATGOV-----TFDV	164
Db	280	QYARSDYGAPPAALSEGRKAVASCPRRFLPLETPADARLIAIANMGKCEDEFGVKGAVDL	339
OY	165	DRDGE----DWNSNSGPPIVANGVTVAG----STCOXSPFCFPVSHGSDATGEELRNRY	216
Db	340	TAGLGPTPGGYISTSPAAYTRNLVIIGHVTINDNSTMEPSG-VIRAFVDHDKLV-NM	397
OY	217	FIPRAGEEGDETGNDYEARMWTGAWGITYPDVTNLVHGSTAVGPASETORG---TPG	273
Db	398	DCGNPDETBEPLAGKEY--TRANSPNMWSLASVEKLGQVY---LPLGNOMPDOMGNGNRTPG	453
OY	274	GTLXGTTIRRAVPDPDGEIYWRHQTLPRBNMOECTFEAMVTNVDOVPSTEMEGLSINP	333
Db	454	AERFSAGL-VALDINTGKLKNNTQPTHHDLMMD-----VGSQPTL-----LDL	496
OY	334	NAATGERERVLTGPCKTGTMMOFDAETG-----	361
Db	497	KTAGVCAFPALI-APTQKSLIYVLDREDDGPPIVIREVAPQAGAVEGHHTAFTAQRSDDL	555
OY	362	-----EFIMA-----RDITYQNMIIESIDENGIVTYNEDAILKEIDVEDV	401
Db	556	LRPPLTERDMWGSSPEFDMLCRIOFSLRYEQGYTPPSQGS�-----I	599
OY	402	CPTFLGRDMPALSANDSGIFYETPLANNVCYDMAVAODEFT---SMDYNTSNVTK----	454
Db	600	YPNAVGVPMNGVSVADVROILFTSPNYAFVSQAMPKPKVYSSGKRGEFTSGVQPNPGA	659
OY	455	-----LPPGKMIGRIDAIDISTGRILMSVERAAA-nyspv-----	489
Db	660	PYAIVMHPPSPILGPLQOARDSCWDGVIDELTTAKVWQHKNGTSBDNPVIGLTVGPS	719
OY	490	----LSTGGCYLVNGCT-DYFFRALSOEGETIMQRLATVASGQA---ISYE-YDGOMQV	541
Db	720	MGGSIITTAGGVAFLSGTLDLYLRAYVKKOKOLMQARLP--AGGQATPMSTYTGKRGROYV	777
OY	542	AI-AGGGVSYSGLSALSALAGERVDSITAIGNAVVEAFLPQ	579
Db	778	LIVAGGHGSGF-----TRMGDIYIAVLAPR	802
 RESULT_12			
ID	P95466	PRELIMINARY; PRT; 786 AA.	
AC	P95466:		
DT	01-MAY-1997 (TREMBLere1_03, Created)		
DT	01-MAY-1997 (TREMBLere1_03, Last sequence update)		
DT	01-JUN-2000 (TREMBLere1_14, last annotation update)		
DE	GLUCOSE DEHYDROGENASE [PYRROLOQUINOLINE-QUINONE] (EC 1.1.99.17).		
GN	GDH.		
OS	Pantoea citrea.		
OC	Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;		
NCBI	taxid=53336;		
RN	[1]		
RP	SEQUENCE FROM N.A., AND ACTIVITY.		
RC	STRAIN=1056r;		
RX	MEDLINE=97133947; PubMed=8979341;		
RA	Cha J.-S., Pujol C., Kado C.I.;		
RT	"Identification and characterization of a Pantoea citrea gene encoding		

RT glucose dehydrogenase that is essential for causing pink disease of
RT pineapple.
RL Appl. Environ. Microbiol. 63:71-76(1997).
CC -1- CATALYTIC ACTIVITY: D-GLUCOSE + ACCEPTOR = D-GLUCONO-1,5-LACTONE +
CC REDUCED ACCEPTOR.
CC -1- CORRECTOR: P00.
CC -1- SUBCELLULAR LOCATION: PERIPLASMIC (BY SIMILARITY).
CC -1- MISCELLANEOUS: RESPONSIBLE FOR PINK TO BROWN DISCOLORATIONS OF
CC INFECTED PINEAPPLES UPON HEATING DURING THE CANNING PROCEDURE.
CC INFECTED BATCHES HAVE TO BE DISCARDED.
CC -1- SIMILARITY: BELONGS TO THE BACTERIAL P00 DEHYDROGENASE FAMILY.
DR EMBL: X85965; CA65229.1;
DR InterPro: IPR001479;
DR InterPro: IPR002372;
DR Pfam: PF01011; Bacterial_P00_1;
DR PROSITE: PS00363; BACTERIAL_P00_1;
DR PROSITE: PS00364; BACTERIAL_P00_2; 1.
KW Oxidoreductase; P00; Transmembrane; Periplasmic.
FT DOMAIN 1 13 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 14 55 POTENTIAL.
FT DOMAIN 56 59 PERIPLASMIC (POTENTIAL).
FT TRANSMEM 60 80 POTENTIAL.
FT DOMAIN 81 85 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 86 106 POTENTIAL.
FT DOMAIN 107 115 PERIPLASMIC (POTENTIAL).
FT TRANSMEM 116 136 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 137 431 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 432 452 POTENTIAL.
FT DOMAIN 453 652 PERIPLASMIC (POTENTIAL).
FT TRANSMEM 653 673 POTENTIAL.
FT DOMAIN 674 700 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 701 721 POTENTIAL.
FT DOMAIN 722 786 PERIPLASMIC (POTENTIAL).
FT TRANSMEM 724 770 POTENTIAL.
FT ACT SITE 462 462 BY SIMILARITY.
SQ SEQUENCE 786 AA; 86038 MW; 372402AAD8B67CC CRC64;

Query Match 10.5%; Score 324.5; DB 2; Length 786;
Best Local Similarity 22.7%; Pred. No. 1.3e-14;
Matches 170; Conservative 91; Mismatches 240; Indels 247; Gaps 36;

QY 2 KPTSLIMASAGALLAALPAFAO-----VPTVDLLANP-----AGEWISYQGNQ 48
DB 115 KFLAMVIGLGINALLLGLASLHPQETNGVLYNSDK---PPASASADWPAYGRQ 170
QY 49 EYRHSPLTOITTEVNGQLVW-----ARGMQPGAV---QVPLHIDGVYLANPQDV 99
DB 171 EYRHSPLTOITTEVNGQLVW-----ARGMQPGAV---QVPLHIDGVYLANPQDV 99
QY 100 IOAIDAKTGDLIWEHRQLPNIAI-----LNSFGEPTRGALVGYVYFVSW 146
DB 231 LIALDAASGRKWRFPDLKSDPTFQHTTCGVSYHEIKSVQSSAPAACSRIFLPVD 290
QY 147 DNHLVALDTATGQVTFVDVROGEGEDMSN-----SSGPVIANG--VIVAGSTCQ 193
DB 291 DGRFAVVALTGORSNF--ANNGETLNLQHPNAYPGGEPTSPILITDKVVIAGSVTD 349
QY 194 -----YSPGCVSGHDSATGELMKNYPIPRAGE-----EGDETNGWDYARAKMTGAWG 243
DB 350 NLSIREPSG-VIRGFDIDSGKILM--VFDPGAKDPNAPVAGQGFVANS-----PNSMA 400
QY 244 QITVDPTNLVHYGSTAVGPASETORGTPGTLGTNTREAVRPDT--GETVMRHQTLPR 301
DB 401 PAADVAQNDIILYLP-----MGVST-----PDINGGAVTRKRWLPA 436
QY 302 DNM---DOCTEFEMAVTNVDQSTEGLOSINPNA-----TGERRVILGVPCCKTGM 353
DB 437 VYVLCMPQALSMHGFTRRYTQMSFMDM-LPS-OPTLADITDEGKIVPVYVPAKIGNI 494
QY 354 WQPAETGE-FLMARDT-----NYQMIISIDENGIVGVYVNEED 389
DB 495 FVLNKGDKPVVPAETFPVPOGPAKGDLSPOTPSSELTFRPKNKLOGRDMWG-ATWEDQ 553

QY 390 ALKRL--DVEYD-----VCPTFLGGRDMSALNPDSGIYFIPLNVCYDM 435
DB 554 LMCRIEHLKREGEPTPPSPSEOGTLVFPDGFMEWGISVN----- 595
QY 436 AVDOETSMYNTSNVTKL-----PPGKD----- 460
DB 596 -TDQFALANMAMFISKLIPRGPNIEFGALGAGSGSEGVQIMYGVPELNP 654
QY 461 -----MIGRIDALISTGRILMSVERAANYS-PV-----LSTGG 494
DB 655 LSPGLPCLQPSMGFVSALNRNHQILMKRIGTRPSAPVPLPFKMGVPMLGPTTAG 714
QY 495 GVLNFGCF-DRYFPALSGEETLMORNLAVASGA--ISYEDNGQYAI-AGGSVY 550
DB 715 NIFVAGLIDNYLRAVYSDGKILMQALP--AGGQATPMTEYDKQYVIMAGHGHSF 772
QY 551 GSGINSALAGERVDSIAGNVYFALP 578
DB 773 G-----TRLGOSLIVKLP 786

RESULT 13
ID 052551 PRELIMINARY; PRT; 644 AA.
AC 052551;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE DEHYDROGENASE.
GN PVAA.
OS Pseudomonas sp.
OC Bacteria; Proteobacteria.
OX NCBI_TaxID=306;
RN [1]
RP SEQUENCE FROM N.A.
RA Matsumiya A., Hatemake T., Tsuji M., Takakura K., Takizawa N.,
RA Kiyohara H.,
RT "Molecular Cloning and Nucleotide sequence a Gene that Encoding
RT Poly(Vinyl alcohol) Dehydrogenase from Pseudomonas sp. 113p3."
RL Submitted (MAR-1996) to the EMBL/Genbank/DBJ databases.
DR EMBL: D83772; BAA12104.1;
DR InterPro: IPR00345;
DR InterPro: IPR002372;
DR InterPro: IPR003088;
DR Pfam: PF00344; Cytochrome_c; 1.
DR Pfam: PF01011; Bacterial_P00_1;
DR PROSITE: PS00190; CYTOCHROME_C; 1.
SQ SEQUENCE 644 AA; 69324 MW; 9D817A59DDAA5303 CRC64;

Query Match 9.1%; Score 281.5; DB 2; Length 644;
Best Local Similarity 24.0%; Pred. No. 1e-11;
Matches 144; Conservative 78; Mismatches 218; Indels 161; Gaps 30;

QY 7 LMASAGALLAALPAFAOAV--TPVTDLLANPAGSEISYSGOENYRHSPLTOITTEWG 65
DB 124 IKGNSVEGTPLADPQSSAPTV--DLGA---ANQNGWSTEDNGRFRKALDVADIP 178
QY 66 QIQLVNARGQPKGVOTPLHIDGVYLANPQGDVIOAIDAKTGDLIWEHRQ-----LPNI 121
DB 179 KKLKMA-PQYPSKNGQATVIGDRLETTSGAVYALNAKGVYWRHRREARTSPVI 237
QY 122 ATINSFCEPLRGALVGNVYFVSWNDNLVALDTATG-----QVTFVDVDRG 167
DB 238 AALPE-----ARHKTALFESDFTKAVALDAETGKOLMTVVDDQPALOMTGSITW 289
QY 168 OGEDWYNSGSPVIANGVIVASSTOYSPFGFVSQSDATGEELMRNFI--PR---A 221
DB 290 DGRITVPISSG-TEAPAQIPTECCAFR--GALVA-LDAATGKILMKRTTTEQEPREKL 345
QY 222 GEGDETNGNDYEARWMTGAWGQITVDPTNLVHYGSTAVGPASETORGTPGTLGTNT 281


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Db 346 NKAGROMGPGGAIWTP-----TVDEARLIYGT-----SNSTIYV---YNSDS 391
QY 282 RFAVRPTGELIWRHQTLPDNDDECTFEMMTNVVDPSTEGLOS-INPNAATGER 340
Db 392 VMAIDADTGAIVTVOGLADNVIIDGCM-----QKGKEHIANPNLPGDPFSIGRA 441
QY 341 RVL-----TGV-PCKGTGMQFPAETGEFLMA--RDTNTQNMIESIDENGIVTNEDAI 391
Db 442 PYLEDGGRKCVSPCR-----AEIGHDLIRAFRPTFRARRE-----478
QY 392 LKEIDVEXDVCPTFLGGRDMPALNDPSGIYFPLNNVCYDMMAYDQETSMVNTSN 451
Db 479 -RQSL-----GSLGMEGTAA---DQKVYAGVSDIA--SOAKDRG-----516
QY 452 VTKLPGKMGIRIDAIDISTGRTIWSVERAA-----ANYSPLSTGGVLFN 499
Db 517 -----KPG-----LMALDIRTGEYAMNFLNAPDKCRNMNMWCHGARSQASIVIPAFIFA 566
QY 500 GGTDRYFRALSQETGELMQ-----TRLATYASGCAISYEVDGMQYVLAAGGVSYSGLN 555
Db 567 GSYGHRFAFPTATGKIIMVDGTGKAVTTLG-----AKAFGGVMDGAGR 613
QY 556 S 556
Db 614 S 614

RESULT 14
P77931
ID P77931 PRELIMINARY; PRT: 639 AA.
AC P77931;
DT 01-FEB-1997 (TREMBLrel. 02, Created)
DT 01-FEB-1997 (TREMBLrel. 02, last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, last annotation update)
DE POO-DEPENDENT POLYVINYL ALCOHOL DEHYDROGENASE PRECURSOR
(FC 1.1.99.23).
GN PVA.
OS Pseudomonas sp.
OC Bacteria; Proteobacteria.
OX NCBI_TaxID=306;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=VM15C;
RX MEDLINE=96376165; PubMed=8782398;
RA Shimao M., Tamogami T., Nishi K., Harayama S.;
RT "The gene pva encodes oxidized polyvinyl alcohol hydrolase of
RT Pseudomonas sp. strain VM15C and forms an operon with the polyvinyl
RT alcohol dehydrogenase gene pvaA."
RL Microbiology 146:649-657(2000).
DR EMBL: D50670; BAA09321.1; -.
DR EMBL: AB008494; BAA94193.1; -.
DR InterPro: IPR000345; -.
DR InterPro: IPR002372; -.
DR InterPro: IPR003088; -.
DR Pfam: PF00034; cytochrome_c_1.
DR Pfam: PF01011; Bacterial_POO; 5.
DR PROSITE: PS00190; CYTOCHROME_C; 1.
KW Signal; Oxidoreductase; POO.
FT SIGNAL 1 33 POTENTIAL.
SQ SEQUENCE 639 AA; 68049 MW; 406E9EF873963B8A CRC64;

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Query Match 9.0%; Score 276.5; DB 2; Length 639;
Best Local Similarity 22.4%; Pired. No. 2.3e-11;

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Matches 143; Conservative 70; Mismatches 241; Indels 183; Gaps 28;
QY 7 LMASAGALLAAPAAQVPTDELLANPAGEWISYQONENYHSPLOTITENNGO 66
Db 117 IWGPSPASMPIDSPKCKKIPPID--LSTP--DQWNGWAGITNRFGQNPGLTADVR 172
QY 67 LQIWMARGMPGKVQVTPILHDCVMTLANPGVIOAIDAKTGLIWEHRQLPNIATLS 126
Db 173 LKYMAMFN-YPGSKNQAVTVGDRLEFVTSMSGAVYALNAKTGCYVRHDAATAATSSVAV 231
QY 127 FGSPTGMLALGYNVEFVMDNLVALDTATG---QVFEDVDRG-----QGEEM 172
Db 232 VOLPAGAPQYA--IFSPWTKAAYALDAQGTQOLKTTIDQPGVOMTGSPTYHDKLP 289
QY 173 VSNSSGPIYANGVYAGSTQCYSPFCFVSGHDSATGEELMKNYFIP-----RAGEED 226
Db 290 VPISSG---NEAFANNQDWECKFRGALVALDLGKVLKMTYTTQKRAPAPRLNKLK 345
QY 227 ETWGNDEYKRMGTGA--WQIITYDPVTNLV-----HYGSTAVGPASETQRTP 272
Db 346 OMWG-----PAGSIMGAPTIDPKRGLVYVATSNSTYEVHSGSDAV-----387
QY 273 GTLTGCTNTRFAVRPTGELIWRHQTLPDNDDECTFEMMTNVVDPSTEGLOSIN 332
Db 388 -----MAEITGKVRMINQYTKDNTITGCP--RANCP-----EKVG 424
QY 333 PNAATGERRVL-----TGVPCKTGTMOQDAET-GEFLMADNTYNNMIESIDENG 382
Db 425 PDEALGNPILHTLDGCRGIYVQKSGAVYAMPDNDSEILWMR-----469
QY 383 IYTNEDAILKELDEYDVCPTFLGGRDMPALNDPSGIYFPLNNVCYDMMAYDQET 442
Db 470 -----RVSPGSEL--GGEV-----GMAADAE--489
QY 443 SMDVY-NTSNVTKLPKPGKMIGRIDAIDISTGRTIWS--VEEAANY-----SPVL 490
Db 490 --NVYGISDVITRKGKRP--GYVALRIDADVAPRPAPTRPCRMNIFCHPAVSQAV 544
QY 491 STGGGVLPNGGTDYRFRALSQETGELMQTRLA-----TVASGOAISYEVDGMQYVLAAG 545
Db 545 TAMPGVYFAGSMDGHRFRASTSDGKIVMEFNAAAPRYKVAOKDQGMDSAG-PTIAG 603
QY 546 GGVSYSGSLNSALAGERVDSTA-----IGNAVYVAL 577
Db 604 GMVYVHSG-----YAGRSTQAGDLRGEGNVLAIFSV 636

RESULT 15
ID 030326 PRELIMINARY; PRT: 470 AA.
AC 030326;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, last sequence update)
DT 01-JUN-2000 (TREMBLrel. 14, last annotation update)
DE GLUCOSE DEHYDROGENASE-A [PYRROLOQUINOLINE-QUINONE] (EC 1.1.99.17)
GN GDHA.
OS Acetobacter europaeus.
OC Bacteria; Proteobacteria; alpha subdivision; Acetobacteraceae;
OX Gluonacetobacter.
OX NCBI_TaxID=33995;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DSM 6160;
RX MEDLINE=97385083; PubMed=9238099;
RA Thurner C.A., Vela C., Theony-Meyer L., Melle L., Teuber M.;
RT "Biochemical and genetic characterization of the acetaldehyde
RT dehydrogenase complex from Acetobacter europaeus."
RL Arch. Microbiol. 168:81-91(1997).
CC -I- CATALYTIC ACTIVITY: D-GLUCOSE + ACCEPTOR = D-GLUCONO-1,5-LACTONE +
CC + REDUCED ACCEPTOR.
CC -I- COFACTOR: POO (BY SIMILARITY).
CC -I- SUBUNIT: MONOMER (BY SIMILARITY).

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CC -1- SUBCELLULAR LOCATION: PERIPLASMIC (BY SIMILARITY).
CC -1- SIMILARITY: STRONG TO OTHER POO GLUCOSE DEHYDROGENASE, LOWER TO
CC METHANOL DEHYDROGENASE SUBUNIT 1, AND TO A. ACETI ETHANOL
CC DEHYDROGENASE.
DR EMBL: Y08696; CAA69952.1; -
DR InterPro: IPR001479; -
DR InterPro: IPR002372; -
DR Pfam: PF01011; Bacterial_POO_5.
DR PROSITE: PS00363; BACTERIAL_POO_1; 1.
DR PROSITE: PS00364; BACTERIAL_POO_2; 1.
KW Oxidoreductase; POO; Periplasmic.
FT NON_TER 1 1
FT ACT_SITE 145 145 BASE (POTENTIAL).
SQ SEQUENCE 470 AA: 50922 MW: 369B73FE24FABBE1 CRC64:

Query Match 7.1%; Score 218; DB 2; Length 470;
Best Local Similarity 21.6%; Pred. No. 1.9e-07;
Matches 110; Conservative 61; Mismatches 176; Indels 162; Gaps 23;

QY 176 SSGPIYAN-GVIYAGS-TCQYS---PFGCFVSGHDSATGEELW-----RN 215
DB 15 TSPPVYDTTIVSGAVTDNYSIHPSG-VTRGFDVHTGALKWAFDPGNDFNEMPSHH 73
QY 216 YELPRAGEGDETWGNDYARMTGAWQITDPTNLVHGSTAVGPASETQRTPGGT 275
DB 74 TRVPSNPSN-----WITS-----STDANDLVYT-----PMGVQTPDIWGN 110
QY 276 LYGTNTRF-----AVRPDTEIIVWRHOTLPNDWDECTFEMMVTNVDPSTEMEGLOS 330
DB 111 RGADAEVYASSTVALNASTGKLWVSQTVHDLMD-----IPAQPSL----- 154
QY 331 INPNAATGERRVLTVGVCCTGTMTWQDAETGEFL-----WARDTNYQNMIESIDE 380
DB 155 VDIRNQGEEVPTLYAPAKTGNIFVLDNRHGLVYPAPERPVQGAPEGDHVSPTQPSQ 214
QY 381 NGIVTVNEDAILKELD-----VEYD-----VCPTFLGGRD 410
DB 215 ---LTFRPSKLLTDADMGGTMYDQLVCRIMFRLRYDGTFTPPSLQGLVFPNGLMFE 271
QY 411 WPSAALNP-----DSGIVFI-----PLNNVCYDM-----MAVDOEF--TSMD 445
DB 272 WGLAVDPVRQIAIANPIAIPFVSRLIPRGPNNPATPKSLPSGSESGVQPFQVPGVD 331
QY 446 VNTSVNTKLPKGMIGRIDAIDISTGRTIMS-----VERAANYSPVL 490
DB 332 LHPFLSPFGLPCKQPAWGMYSGLDLRTNKIWKHNRGTIRDSAPLPLPKMGVPSLGGPL 391
QY 491 STGGGVLFNGGT-DRYFRALSOETGETLQTRLATVASGOAISYEVDGMQYVAIAGGVS 549
DB 392 TTAGGAFLTLSTLDYIRAYDVTNGHVLMDRLPAGGOSTPMTYAVDQKQYIVTADGC-- 449
QY 550 YSGGLNSALAGERVDSSTAIGNAVVFPALP 578
DB 450 HGS-----FGTKLGDYIVAVSLP 467

Search completed: August 8, 2001, 19:43:52
Job time: 194 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: August 9, 2001, 10:10:01 ; Search time 72.18 Seconds
(without alignments)
4563.610 Million cell updates/sec

Title: US-08-934-506A-1
Perfect score: 1740
Sequence: 1 ATGAACCGACTGCTGCT.....TCTTCGCCCTGCCCAATTA 1740

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 324599 segs, 94655562 residues
Total number of hits satisfying chosen parameters: 649198

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents_NA:*
1: /cgn2_6/prodata/1/lna/5A_COMB.seq:*
2: /cgn2_6/prodata/1/lna/5B_COMB.seq:*
3: /cgn2_6/prodata/1/lna/6A_COMB.seq:*
4: /cgn2_6/prodata/1/lna/6B_COMB.seq:*
5: /cgn2_6/prodata/1/lna/PCRTUS_COMB.seq:*
6: /cgn2_6/prodata/1/lna/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	92.2	5.3	2214	1	US-07-985-458-1
2	76.2	4.4	2163	4	US-09-286-284-22
3	76.2	4.4	2265	4	US-09-286-284-1
4	76.2	4.4	4830	4	US-09-286-284-7
5	42.2	2.4	2745	1	US-08-363-255-1
6	42.2	2.4	2745	1	US-08-363-255-13
7	41.4	2.4	655	1	US-08-471-119A-5
8	40.2	2.3	44377	2	US-08-804-227C-7
9	40.2	2.3	44377	2	US-08-804-198-1
10	39.8	2.3	1164	1	US-07-640-476-6
11	39.4	2.3	3748	2	US-08-686-417-2
12	39.4	2.3	36519	3	US-08-923-137-2
13	39.4	2.3	5515	4	US-09-398-193-08
14	38.8	2.2	20235	1	US-07-642-734C-3
15	38.8	2.2	20235	1	US-08-439-009A-3
16	38.4	2.2	2004	1	US-08-471-033-18
17	38.4	2.2	2004	2	US-08-471-044-18
18	38.4	2.2	2004	2	US-08-463-483A-18
19	38.4	2.2	2004	2	US-08-471-046A-18
20	38.4	2.2	2004	2	US-08-470-566B-18
21	38.4	2.2	2004	2	US-08-469-334-18
22	38.4	2.2	2004	3	US-09-300-529-18
23	38.4	2.2	2576	2	US-08-471-033-35
24	38.4	2.2	2576	2	US-08-471-044-35
25	38.4	2.2	2576	2	US-08-463-483A-35
26	38.4	2.2	2576	2	US-08-471-046A-35
27	38.4	2.2	2576	2	US-08-470-566B-35

28	38.4	2.2	2576	2	US-08-469-334-35	Sequence 35, Appl
29	38.4	2.2	2576	3	US-09-300-529-35	Sequence 35, Appl
30	38.4	2.2	2655	1	US-08-471-033-17	Sequence 17, Appl
31	38.4	2.2	2655	1	US-08-471-033-26	Sequence 26, Appl
32	38.4	2.2	2655	2	US-08-471-044-17	Sequence 17, Appl
33	38.4	2.2	2655	2	US-08-471-044-26	Sequence 26, Appl
34	38.4	2.2	2655	2	US-08-463-483A-17	Sequence 17, Appl
35	38.4	2.2	2655	2	US-08-463-483A-26	Sequence 26, Appl
36	38.4	2.2	2655	2	US-08-471-046A-17	Sequence 17, Appl
37	38.4	2.2	2655	2	US-08-471-046A-26	Sequence 26, Appl
38	38.4	2.2	2655	2	US-08-470-566B-17	Sequence 17, Appl
39	38.4	2.2	2655	2	US-08-470-566B-26	Sequence 26, Appl
40	38.4	2.2	2655	2	US-08-469-334-17	Sequence 17, Appl
41	38.4	2.2	2655	2	US-08-469-334-26	Sequence 26, Appl
42	38.4	2.2	2655	3	US-09-300-529-17	Sequence 17, Appl
43	38.4	2.2	2655	3	US-09-300-529-26	Sequence 26, Appl
44	38.4	2.2	3407	1	US-08-253-155A-7	Sequence 7, Appl
45	38.4	2.2	4031	1	US-08-471-033-49	Sequence 49, Appl

ALIGNMENTS

RESULT 1
US-07-985-458-1
Sequence 1, Application US/07985458
Patent No. 5344777
GENERAL INFORMATION:
APPLICANT: Takemura, Toshimi;
APPLICANT: Takemura, Hiroshi;
APPLICANT: Tayama, Kenji;
APPLICANT: Fukaya, Masahiro;
APPLICANT: Okumura, Hajime and
APPLICANT: Kawamura, Yoshiya
TITLE OF INVENTION: Structural Gene of Membrane-Bound
TITLE OF INVENTION: Alcohol Dehydrogenase Complex, Plasmid
TITLE OF INVENTION: Containing The Same And Transformed Acetic Acid
TITLE OF INVENTION: Bacteria
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSER: Frischauf, Holtz, Goodman & Woodward, P.C.
STREET: 600 Third Avenue
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10016-2088
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 0.72 mb
COMPUTER: IBM PC compatible (NEC PC-9801 ES)
OPERATING SYSTEM: MS DOS
SOFTWARE: ASCII Form
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/985,458
FILING DATE: 19921203
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/658,221
FILING DATE: 20-FEB-1991
APPLICATION NUMBER: 73440/1990
FILING DATE: 26-MAR-1990
ATTORNEY/AGENT INFORMATION:
NAME: Goodman, Herbert
REGISTRATION NUMBER: 17081
REFERENCE/DOCKET NUMBER: 910134/HG
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)972-1400
TELEFAX: (212)370-1622
TELEX: 236268
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2214 base pairs
TYPE: nucleic acid
STRANDEDNESS: double

1 TOPOLOGY: unknown
 2 MOLECULE TYPE: genomic DNA
 3 ORIGINAL SOURCE:
 4 ORGANISM: *Acetobacter altoacetigenes*
 5 STRAIN: M-24
 6 PUBLICATION INFORMATION:
 7 AUTHORS: Tamaki, Toshimi;
 8 AUTHORS: Fukaya, Masahiro;
 9 AUTHORS: Takemura, Hiroshi;
 10 AUTHORS: Tayama, Kenji;
 11 AUTHORS: Okumura, Hajime;
 12 AUTHORS: Kawamura, Yoshiya;
 13 AUTHORS: Nishiyama, Makoto;
 14 AUTHORS: Horinouchi, Sueharu and
 15 AUTHORS: Beppu, Teruhiko
 16 TITLE: Cloning and Sequencing of the Gene Cluster
 17 TITLE: Encoding Two Subunits of Membrane-Bound
 18 TITLE: Alcohol Dehydrogenase from *Acetobacter*
 19 TITLE: *polyoxogenes*
 20 JOURNAL: *Biochimica et Biophysica Acta*.
 21 VOLUME: 1088
 22 PAGES: 297-300
 23 DATE: 1991
 24

Query Match	5.38;	Score 92.2;	DB 1;	Length 2214;
Best Local Similarity	55.0%;	Pred. No. 1.2e-13;		
Matches 225; Conservative	0;	Mismatches 178;	Indels 6;	Gaps 2

[illegible]

RESULT 2
US-09-296-284--22
Sequence 22, Application US/09296284A
Patent No. 6204040
GENERAL INFORMATION:
APPLICANT: Choi, Eun-Sung
APPLICANT: Rhee, Sang-Ki
APPLICANT: Lee, Eun-Hae
TITLE OF INVENTION: Glucobacter Suboxydans Sorbitol Dehydrogenase, Genes
TITLE OF INVENTION: and Methods of Use Thereof
FILE REFERENCE: 1533.0870000
CURRENT APPLICATION NUMBER: US/09/296,284A
CURRENT FILING DATE: 1999-04-22
NUMBER OF SEQ ID NOS: 87

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; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 22
; LENGTH: 2163
; TYPE: DNA
; ORGANISM: Gluconobacter suboxydans
US-09-296-284-22

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Query Match	4.48;	Score 76.2;	DB 4;	Length 2163;
Best Local Similarity	52.9%;	Pred. No. 9.5e-10;		
Matches 212; Conservative	0;	Mismatches 183;	Indels 6;	Gaps 2

QY 100 GGGAAACCGGCCCCGCTGGTGGATGTGATTCAGCTACGGTTCAGAACCAAGAAAACCTACCGCTCAC 159

Db 28 gccgaccgacatcccggtgtgactgagtgaatgacatgagccgacactcttcgagcagcgtcac 87

QY 160 TCGCCCCCTGACGCACATATCAGCATGTAGACAACTCCGGCCAACTGCACAACTGGTCTGGGGCGCG 219

Db 88 agccgcgcgtgatcgaatcaccaagaagacaaatcgagacatctgaagccgtgcacatgagcaactac 147

QY 220 GGCATGACGACCGGGGCAAAAGTCC---AACTCAGGCCCTGTATCCATGACGGCGTCATGTAT 276

Db 148 gatctgataccaacacgctgctcagaagaagctacgcgtctgattcgttggctgcatagttac 207

QY 277 CTGGCAAAACCCGGGGAGCGATATCTCAGGCCATTCAGCCCAAAACTGGCCATCTGATCTGG 336

Db 208 gccacacaaacatctgagagaagaattgaagctctgattgcagctacgcgcgaagcgtcgttgg 267

QY 337 GAACACCGCCGCCCAACTGCC---GAACATCGGCCACGGCTGAACAGCTTTGGCGAGCGCGACC 393

Db 268 tcttcagatccaagaaggttccagagcaaacatcgccgacccgctgcgtgcgtatcagttcaac 327

QY 394 CGCGGCGATGGCGCTGTACGGCACCACAGTTACTTTGTTCTGTTGGCAACAACCACTCGGTG 453

Db 328 ctgtgtgcagactactgaaacgcaaaagtctatttcgcaaccttcgaagcgtgcgcgtatt 387

QY 454 GCCCTCGACACCGCAACTGGCGCAAGTACGTTGCAGCTGCA 494

Db 388 gccctggtatgccaaagaccgaagaacgtgtctgttgaagcgttca 428

```

RESULT      3
US-09-296-284-1
: Sequence 1, Application US/09256284A
: Patent No. 6204040
: GENERAL INFORMATION:
: APPLICANT: Choi, Eun-Sung
: APPLICANT: Rhee, Sang-Ki
: APPLICANT: Lee, Eun-Hae
: TITLE OF INVENTION: Glucobacter Suboxydans Sorbitol Dehydrogenase, Genes
: TITLE OF INVENTION: and Methods of Use Thereof
: FILE REFERENCE: 1533.0870000
: CURRENT APPLICATION NUMBER: US/09/256,284A
: CURRENT FILING DATE: 1999-04-22
: NUMBER OF SEQ. ID NOS.: 87
: SOFTWARE: PatentIn Ver. 2.0
: SEQ. ID NO. 1
: LENGTH: 2265
: TYPE: DNA
: ORGANISM: Glucobacter suboxydans
: US-09-296-284-1

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Query Match	4.4%	Score 76.2	DB 4	Length 2265	
Best Local Similarity	52.9%	Pred. No. 9.6e-10			
Matches 212	Conservative	0	Mismatches 183	Indels 6	
			Gaps	2	
QY	100	GCGAACC	CGCCCGCTGGTG	GAATGATCAGTCACGCTAGAGAACAAGAAATACCTGCAC	159
Db	130	gcccagcagc	atcgcggtgactcgtgtgcctatgctccgagacctatctccgcgcgctac	189	
QY	160	TGCCCCCTTACG	CAATCAGCATCAGACTAGAGAGCTGGCCAACTGC	CAATGCTTGGGGCGCC	219

Db 190 agcccgctgagatcagatccacaagacatgagcaatctgaagctgagctgactac 249
QY 220 GGATGACAGCGGGCAAGTCC---AAGTACAGCCCTGATCCATGACGGCGTCATGTAT 276
Db 250 gatctgataccaacgctggtcaggaagtagcagcctgactgctgagctgac 309
QY 277 CTGGCAAAACCGGCGAGCATGATCCAGGCGCAAACTGGCGGATGATCTG 336
Db 310 gccacacaacatgaggaagaaagctctgagtagcagctgagcaagctgctgag 369
QY 337 GAACACCGCGCCCAACTGCC---GAACATGCGCACGCTGAACAGCTTTGGCAGACG 393
Db 370 tcttaagatccaaaggttccaggaacatcgcgacgcgctgctgagtagcagctaac 429
QY 394 CGCGGCAATGGCGCTGTACGGCACCACGTTTACTTTGTTTGTGGGACAACACTGTGTC 453
Db 430 cgtgtgtagcagctactgagcaagcgaatctatttcgcaaccttcgagcagctgctgatt 489
QY 454 GCCCTGACACCGCAACTGGCAGTGCCTTGACGTCGA 494
Db 490 gccctgagtagcagaagcagcagctgctgagcgtcta 530

RESULT 4

US-09-296-284-7
Sequence 7, Application US/09296284A
Patent No. 6204040
GENERAL INFORMATION:
APPLICANT: Choi, Eun-Sung
APPLICANT: Rhee, Sang-Ki
APPLICANT: Lee, Eun-Hae
TITLE OF INVENTION: Glucobacter Suboxydans Sorbitol Dehydrogenase, Genes
FILE REFERENCE: 1533.0870000
CURRENT APPLICATION NUMBER: US/09/296,284A
CURRENT FILING DATE: 1999-04-22
NUMBER OF SEQ ID NOS: 87
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 7
LENGTH: 4830
TYPE: DNA
ORGANISM: Glucobacter suboxydans
US-09-296-284-7

Query Match 4.4%; Score 76.2; DB 4; Length 4830;
Best Local Similarity 52.9%; Pred. No. 1.2e-09;
Matches 212; Conservative 0; Mismatches 183; Indels 6; Gaps 2;

QY 100 GCGAACCAGCGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 159
Db 794 gccgacagcagatccggtgtagttagttagttagttagttagttagttagttagttagt 853
QY 160 TCGGCCCCGACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 219
Db 854 agcccgctgagatcaccacgaagcaatgagcaatctgagctgagctgagctgagctgag 913
QY 220 GGCATGACGCGGGCAAGTCC---AAGTACAGCCCTGATCCATGACGGCGTCATGTAT 276
Db 914 gatctgataccaacgctggtcaggaagtagcagcctgactgctgagctgagctgagctgac 973
QY 277 CTGGCAAAACCGGCGAGCATGATCCAGGCGCAAACTGGCGGATGATCTG 336
Db 974 gccacacaacatgaggaagaaagctctgagtagcagctgagcaagctgctgag 1033
QY 337 GAACACCGCGCCCAACTGCC---GAACATGCGCACGCTGAACAGCTTTGGCAGACG 393
Db 1034 tcttaagatccaaaggttccaggaacatcgcgacgcgctgctgagtagcagctaac 1093
QY 394 CGCGGCAATGGCGCTGTACGGCACCACGTTTACTTTGTTTGTGGGACAACACTGTGTC 453
Db 1094 cgtgtgtagcagctactgagcaagcgaatctatttcgcaaccttcgagcagctgctgatt 1153

QY 454 GCCCTGACACCGCAACTGGCAGTGCCTTGACGTCGA 494
Db 1154 gccctgagtagcagaagcagcagctgctgagcgtcta 1194

RESULT 5

US-08-363-255-1
Sequence 1, Application US/08363255
Patent No. 5783386
GENERAL INFORMATION:
APPLICANT: JACOBS, JR., WILLIAM R.
APPLICANT: BLOOM, BARRY R.
APPLICANT: COLLINS, DESMOND M.
APPLICANT: DE LISLE, GEOFFREY W.
APPLICANT: PASCOPELLA, LISA
APPLICANT: KAMAKAMI, RIKU P.
TITLE OF INVENTION: MYCOBACTERIA VIRULENCE FACTORS AND A
TITLE OF INVENTION: NOVEL METHOD FOR THEIR IDENTIFICATION
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/363,255
FILING DATE: 23-DEC-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MONROY, GLADYS H.
REGISTRATION NUMBER: 32,430
REFERENCE/DOCKET NUMBER: 25237-20002.22
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2745 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 835..2424
US-08-363-255-1

Query Match 2.4%; Score 42.2; DB 1; Length 2745;
Best Local Similarity 45.4%; Pred. No. 0.18;
Matches 152; Conservative 0; Mismatches 183; Indels 0; Gaps 0;

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QY 1045 AAACCGGACCATGTGGAGTTCGAGCGCGAAACCGGCGAATTCCTGGGCGCGTAT 1104
Db 1066 AAGACCCCGCGCGCGGCAATCCCGCGCGGAGGACCGTGGCGCGCGCACGCG 1125
QY 1105 ACCAATCAACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1164
Db 1126 ACCAAGCCACGAGCGCGCCAGAGATGCGCAGACGAAAGCCGCAAGAGATCCGAGAGCGCC 1185
QY 1165 GATGCAATCCTGAAGAACTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1224

DB 1186 CTGACCTCCGTGAGAGAGTCGACCGCTGACACGACCTGACGCTGACCGCGGAGGAC 1245
QY 1225 CGGACCTGGCCCTCGCGCGCTGACACCGGAGCGAGCTGATCTATCCCGCTGAC 1284
DB 1246 CTCGACCTTGAGACCGCGCGCTGACACCTGATGACCTGAGAGGACGACGCTGCGCGGAC 1305
QY 1285 AACGCTGCTATGACATGATGAGCGCGATGACGGA 1319
DB 1306 GCCGACGACGACCTGACCTGACGCGGCGACGACGACGGA 1340

RESULT 6
US-08-363-255-13
Sequence 13, Application US/0836255
Patent No. 5783386
GENERAL INFORMATION:
APPLICANT: JACOBS, JR., WILLIAM R.
APPLICANT: BLOOM, BARRY R.
APPLICANT: COLLINS, DESMOND M.
APPLICANT: de Lisle, GEOFFREY W.
APPLICANT: PASCOPELLA, LISA
APPLICANT: KAWAKAMI, RIKU P.
TITLE OF INVENTION: MYCOBACTERIA VIRULENCE FACTORS AND A
TITLE OF INVENTION: NOVEL METHOD FOR THEIR IDENTIFICATION
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/363,255
FILING DATE: 23-DEC-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MONROY, GLADYS H.
REGISTRATION NUMBER: 32,430
REFERENCE/DOCKET NUMBER: 25237-20002.22
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 2745 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 841..2424
FEATURE:
NAME/KEY: misc_difference
LOCATION: replace(937, "")
OTHER INFORMATION: /note="This position is G or C."
OTHER INFORMATION: If it is G the amino acid translation is Ala."
FEATURE:
NAME/KEY: misc_difference
LOCATION: replace(2384, "")
OTHER INFORMATION: /note="This position is A or G."
OTHER INFORMATION: If it is A the amino acid translation is His."
FEATURE:
NAME/KEY: misc_difference
LOCATION: replace(2591, "")
OTHER INFORMATION: /note="This position is C or T."
US-08-363-255-13

Query Match 2.48; Score 42.2; DB 1; Length 2745;
Best Local Similarity 45.48; Pred. No. 0.18;
Matches 152; Conservative 0; Mismatches 183; Indels 0; Gaps 0;

QY 985 CAGTCGATCAACCGAAGCGCGCAACTGCGACGTCGCTGCTGACCGCGTTCCGTGC 1044
DB 1006 CGGTCCGTCGAAGCGCGCGCTGCGGACCGCCAGACACTGACGACGACGACGACGAAAG 1065
QY 1045 AAAACCGGACACATGTTGGCATTTTCGACGCGGAAACCGGCAATTTCTGTGGCGCCGTGAT 1104
DB 1066 AAGACCCCGCGCGCGCGCAATTCGCGCGCGGCAAGGACACGTCGCGCGCGCGCGG 1125
QY 1105 ACCGACCTACCAAGACATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1164
DB 1126 ACCGACCTACCAAGACATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1185
QY 1165 GATGCTGCTGAGAGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1224
DB 1186 CTGACCTCCGTGAGAGAGTCGACCGCTGACACGACGACGACGACGACGACGACGACGAC 1245
QY 1225 CGGACCTGGCCCTCGCGCGCTGACACCGGAGCGAGCTGATCTATCCCGCTGAC 1284
DB 1246 CTCGACCTTGAGACCGCGCGCTGACACCTGATGACCTGAGAGGACGACGTCGCGCGGAC 1305
QY 1285 AACGCTGCTATGACATGATGAGCGCGATGACGGA 1319
DB 1306 GCCGACGACGACCTGACCTGACGCGGCGACGACGACGGA 1340

RESULT 7
US-08-471-119A-5
Sequence 5, Application US/08471119A
Patent No. 5827706
GENERAL INFORMATION:
APPLICANT: Leitner, Ernst
APPLICANT: Schneider, Elisabeth
APPLICANT: Schoerendorfer, Kurt
APPLICANT: Weber, Gerhard
TITLE OF INVENTION: Cyclosporin Synthetase
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 5827706artis Corporation
STREET: 59 Route 10
CITY: East Hanover
STATE: New Jersey
COUNTRY: USA
ZIP: 07936
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,119A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Kassenoft, Melvyn
REGISTRATION NUMBER: 26,389
REFERENCE/DOCKET NUMBER: 100-8029/CONT/CONT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 503 8874
TELEFAX: 201 503 8807
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 655 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO


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1 LOCATION: 97..1482 /function= "approximate span of
2 OTHER INFORMATION: beta-ketoacyl ACP synthase of module 3"
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4 FEATURE:
5 NAME/KEY: misc_feature
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7 OTHER INFORMATION: acyltransferase domain module 3"
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12 OTHER INFORMATION: beta-ketoreductase domain of module 3"
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17 OTHER INFORMATION: acyl carrier domain of module 3"
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22 OTHER INFORMATION: module 4"
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35 NAME/KEY: misc_feature
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40 NAME/KEY: misc_feature
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42 OTHER INFORMATION: beta-ketoreductase of module 4"
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45 NAME/KEY: misc_feature
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47 OTHER INFORMATION: acyl carrier domain of module 4"
48 OTHER INFORMATION:
49 FEATURE:
50 NAME/KEY: CDS
51 LOCATION: 10723..20235 /function= "approximate span of
52 OTHER INFORMATION: /codon_start= 10723
53 OTHER INFORMATION: /function= "gene "eryA"
54 OTHER INFORMATION: /product= "orf3 encoding modules 5 & 6
55 OTHER INFORMATION: 6-deoxyerythronolide B formatto"
56 OTHER INFORMATION:
57 FEATURE:
58 NAME/KEY: misc_feature
59 LOCATION: 10723..15165 /function= "approximate span of
60 OTHER INFORMATION: module 5"
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62 FEATURE:
63 NAME/KEY: misc_feature
64 LOCATION: 10831..12174 /function= "approximate span of
65 OTHER INFORMATION: beta-ketoacylACPSynthase domain of modul"
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75 OTHER INFORMATION:

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Search completed: August 9, 2001, 22:38:11
Job time: 44890 sec

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NAME/KEY: misc_feature
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OTHER INFORMATION: /function= "approximate span of
OTHER INFORMATION: module 6"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 15172..16569
OTHER INFORMATION: /function= "approximate span of
OTHER INFORMATION: beta-ketoacylACPSynthase domain of modul"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 16768..17721
OTHER INFORMATION: /function= "approximate span of
OTHER INFORMATION: acyltransferase domain of module 6"
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NAME/KEY: misc_feature
LOCATION: 18379..18921
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NAME/KEY: misc_feature
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FEATURE:
NAME/KEY: misc_feature
LOCATION: 19492..20235
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US-08-439-009A-3
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Query Match 2.2%; Score 38.8; DB 3; Length 20235;

Best Local Similarity 45.9%; Pred. No. 2.1; Mismatches 197; Indels 1; Gaps 1;

Matches 168; Conservative 0; Mismatches 197; Indels 1; Gaps 1;

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DB 6304 GTAAACCCCGCCCGCGCTGTCGGCCACTCGCAGGGGAGATCGCCGCGCACGTGGCG 6363
QY 394 CGCGGCGATGGCGCTGTACGGCCCAACGTTTACTTTGTTGTTGGACAAACCACTGGTC 453
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 6364 GCGCGCGCTGTGCTGGAAGCGCCGCAAGGTGTGGCCCTGCGCAGCCAGGTGTGGCG 6423
QY 454 GCCTCGACACCGCACTGGCCCAAGTACGTGTGACGTGACCGCGGCCCAAGCGAAGAC 513
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 6424 GAGCTGACGACGACGAGGCGGCGATGTGTGCGCGCGCTCCGCGACGAGCTGAGACC 6483
QY 514 ATGGTTTCGAATCTGTCGGGCGCCGATCGTGTGCAACGGCGTGATCGTTGGCGTTGACG 573
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DB 6484 GTGCTCGCGCGCTGGAGCGCCGCTGTGCGCGTGGCCGCTGTAACGGCGCTGSCACACG 6543
QY 574 TGCCAACTACTCGCGCTTGGCGCTGTTGTCTCGGGCCACGACTCGGCCACCGGTGAAGAG 633
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DB 6544 GTGCTTCCGCGCGGCGGAGCTGAGAGTGTCTTTCGCGAGGCGCGAGCGCGGAG 6603
QY 634 CTGTGGGCGCAACTACTTCAATCCCGCGCTGGGAGAGAGGTATGATGACTTGGGGCAAC 693
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DB 6604 ATGAAGCGCGCGGATCGCGCTGCTACGCTCCACACTCCCGGAGGTGGCGGCAATC 6663
QY 694 GATTAC 699
    || ||
DB 6664 GAGGAC 6669
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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: August 9, 2001, 09:52:11 ; Search time 17754.2 seconds
(without alignments)
926.427 Million cell updates/sec

Title: US-08-934-506A-1

Perfect score: 1740

Sequence: 1 ATGAACCGACTGCTGCT.....TCCTGCCCTGCCGCATATA 1740

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 10228115 seqs, 4726426750 residues

Total number of hits satisfying chosen parameters: 20456230

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_est4:*
5: gb_est5:*
6: gb_est6:*
7: gb_est7:*
8: gb_est8:*
9: gb_est9:*
10: gb_est10:*
11: gb_est11:*
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255: gb_estl75:*
256: gb_estl76:*
257: gb_estl77:*
258: gb_estl78:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	49.2	2.8	298	246	A2577200	A2577200 04g03 Shm
2	49.2	2.8	925	219	CNS0091P	AL053013 Drosophill
3	46	2.6	643	171	BF937817	BF937817 fm68d03.y
4	45.6	2.6	667	175	BG307693	BG307693 fms18d03.y
5	45.4	2.6	925	219	CNS0091P	AL053013 Drosophill
6	43.6	2.5	616	121	AM827060	AM827060 IK57h09.y
7	43.6	2.5	662	175	BG308084	BG308084 fms5f02.y
8	43.6	2.5	641	137	BE602586	BE602586 HVSMEb010
9	43.4	2.5	780	220	CNS02PE9	AL14922 Tetraodon
10	43	2.5	308	164	BE211954	BE211954 894024H07
11	43	2.5	759	166	BF259495	BF259495 HVSMEf001
12	42.8	2.5	880	167	BE456143	BE456143 HVSMEg001
13	42.2	2.4	767	147	BF305223	BF305223 601892676
14	42.2	2.4	553	166	BE364747	BE364747 P11_15.A1
15	41.8	2.4	465	155	BG557222	BG557222 EML_44.B1
16	41.8	2.4	487	167	BE429911	BE429911 TAS005.A1
17	41.8	2.4	641	77	BE214833	BE214833 HV_CEB000
18	41.8	2.4	1101	219	CNS011SY	AL108460 Drosophill
19	41.6	2.4	586	139	BE758607	BE758607 an_3051.A
20	41.4	2.4	839	219	CNS004NB	AL054280 Drosophill
21	41.4	2.4	977	219	CNS003X7	AL076850 Drosophill
22	41	2.4	648	236	AO960102	AO960102 LEREP38FR
23	40.8	2.3	394	155	BG556077	BG556077 EML_66.D0
24	40.8	2.3	476	166	BE364011	BE364011 P11_11.S0
25	40.8	2.3	485	166	BE215238	BE215238 HV_CEB000
26	40.8	2.3	499	155	BG574731	BG574731 EML_44_A0
27	40.8	2.3	513	137	BE559428	BE559428 HV_CEB002
28	40.8	2.3	1101	219	CNS011SY	AL108460 Drosophill
29	40.4	2.3	430	136	BE490518	BE490518 HNE0362.F
30	40.4	2.3	556	136	BE497212	BE497212 WHF0765.F
31	40.4	2.3	680	136	BE470555	BE470555 WHE0261.C
32	40.4	2.3	714	164	BE216552	BE216552 HV_CEB001
33	40.4	2.3	807	167	BE418273	BE418273 SCL023.G0
34	40.4	2.3	878	167	BE417933	BE417933 SCL012.H1
35	40.4	2.3	472	164	BE215276	BE215276 HV_CEB000
36	40.2	2.3	517	136	BE500032	BE215786 HV_CEB000
37	40.2	2.3	517	136	BE500032	BE500032 WHE0977.D
38	40.2	2.3	521	137	BE606263	BE606263 WHE0905.H
39	40.2	2.3	524	167	BE423563	BE423563 WHE0317.G
40	40.2	2.3	528	136	BE49986	BE49986 WHE0977.H
41	40.2	2.3	529	146	BF265039	BF265039 HV_CEA001
42	40.2	2.3	532	136	BE498908	BE498908 WHE0968.D
43	40.2	2.3	554	146	BF263305	BF263305 HV_CEA000
44	40.2	2.3	756	146	BF265359	BF265359 HV_CEA001
45	40.2	2.3	759	146	BF265401	BF265401 HV_CEA001

ALIGNMENTS

[illegible]

REFERENCE 1 (bases 1 to 667)
 AUTHORS Clark, M., Johnson, S.L., Lehrach, H., Lee, R., Li, F., Marra, M., Eddy, S., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Saller, J., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.
 TITLE Mashu zebrafish EST Project 1998
 JOURNAL Unpublished (1998)
 COMMENT Contact: Stephen L. Johnson
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: zbratfish@wustl.edu
 Library constructed by: Susan E. Brockerhoff DNA sequencing by:
 Washington University Genome Sequencing Center Clone distribution:
 Ressourcenzentrum/PrimaDatenbank, Berlin, Germany (web address:
 www.rzpd.de)
 Seq primer: T3 ET from Amersham
 High quality sequence stop: 415.

FEATURES
 source location/Qualifiers
 1..667
 /organism="Danio rerio"
 /strain="wild-type"
 /db_xref="taxon:7955"
 /clone="4199212"
 /clone_lib="zebrafish adult retina cDNA"
 /sex="mixed"
 /dev_stage="1-2 years"
 /lab_host="E.Coli XL1-Blue MRF' (XL1-Blue MRF')"
 /note="Vector: Lambda ZAP II (pbluescript SK-); Site_1:
 EcoRI; Site_2: SalI; This zebrafish library was
 constructed by Dr. Susan E. Brockerhoff (email:
 sbrocker@u.washington.edu) RZPD library number: 760"

BASE COUNT 168 a 180 c 189 g 130 t

ORIGIN

Query Match 2.6%; Score 45.6; DB 175; Length 667;
 Best Local Similarity 48.5%; Pred. No. 0.28;
 Matches 126; Conservative 0; Mismatches 134; Indels 0; Gaps 0;

OY 366 CACGCTGAACAGCTTTGGCGAGCGACCGCGGCGCTGTACGGCAACCACTTTA 425
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 DB 391 CCCGCTGGCGCTCTCGTGGTGAATGAGCTGTGCGTACGCCGCGAAACTACGTGGC 450
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 OY 426 CTTGTTTGTGGGACAACCACTGTGCGCTGTGACACCGCAACTGGCCCAAGTACGTT 485
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 DB 451 GTGCGAGGTTTGGACAACATCTGCTCATCTTACAACTGAAGACCGCGAGGGGAAGT 510
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 OY 486 CGAGCTGACCGCGCGCAAGCGAAGACATGTTTGAACCTGTGCGGCGCGATCTGGC 545
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 DB 511 GCGGCTCAGCGCGGACGCTAGCGGACACAGATTATCTGTCTGCGCTTTCCTGGA 570
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 OY 546 AAACGGCGTGAATCGTGGCGGTTCGACCTGCAATTAATCTGCGCTTGTGCTTC 605
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 DB 571 TGATTAACCAATGTGACAGCTCAGGACACCACTGTGCTGTGGGACATCGAGAC 630
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 OY 606 GGGCCACACACCGCCACCG 625
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 DB 631 TGGCCAGCAGACGACCG 650
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 5
 LOCUS CDS0091P 925 bp DNA GSS 03-JUN-1999
 DEFINITION Drosophila melanogaster genome survey sequence TET3 end of BAC #
 BACR19D16 of Rpci-98 library from Drosophila melanogaster (fruit
 fly), genomic survey sequence.
 ACCESSION AL053013
 VERSION AL053013.1 GI:4934461
 KEYWORDS GSS.

SOURCE
 ORGANISM fruit fly.
 Drosophila melanogaster
 Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
 Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
 TITLE 1 (bases 1 to 925)
 JOURNAL Genoscope.
 COMMENT Direct Submission
 Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
 BP 191 91006 Evry cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
 - Web : www.genoscope.cns.fr)
 Determination of this BAC-end sequence was carried out as part of a
 collaboration with the Berkeley Drosophila Genome Project (BDGP).
 The BDGP is constructing a physical map of the Drosophila
 melanogaster genome using these BACs. For further information
 please see <http://www.fruitfly.org> The BDGP Drosophila
 melanogaster BAC library was prepared by Kazutoyo Oseogawa and
 Aaron Mammoser in Pieter de Jong's laboratory in the Department of
 Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
 NY. The library is named Rpci-98 and was constructed by partial
 EcoRI digestion of Drosophila DNA provided by the BDGP from the
 isogenic strain Y2; cn bw sp, the same strain used for the BDGP's
 pl and EST libraries. A more detailed description of the library
 and how to order individual BAC clones, the entire library, or
 filters for hybridization from the BACPAC Resource Center can be
 found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.

FEATURES
 source location/Qualifiers
 1..925
 /organism="Drosophila melanogaster"
 /db_xref="taxon:7227"
 /clone_lib="Rpci-98"
 /clone="BACR19D16"
 /note="end : TET3"

BASE COUNT 120 a 61 c 61 g 172 t 511 others

ORIGIN

Query Match 2.6%; Score 45.4; DB 219; Length 925;
 Best Local Similarity 13.2%; Pred. No. 0.33;
 Matches 40; Conservative 140; Mismatches 122; Indels 0; Gaps 0;

OY 520 TCGAAGCTGCGGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 579
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 DB 896 BCSSSSBSSBSSSTSSBSSBSSBSSBSSBSSBSSBSSBSSBSSBSSBSSBSSBSSBSS 837
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 OY 580 TACTCGCGCTTCCGCTGCTTGTCTCGCGCCACGACTCGGCGGCGGCGGCGGCGGCGG 639
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 DB 836 CSSSSSSCGSASAGKVRASGAGKRGSGSASASHSSSSBSSSSCSASCSWSSS 777
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 OY 640 CGCACTACTTATCCCGCGCGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 699
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 DB 776 SSSASSSSRSRSGGAGAGSGASSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSS 717
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 OY 700 GAAGCGCGTGTGACCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 759
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 DB 716 MSCSSBSSSASASSSSSSSSSACASCCCTTSMSCSTASMSARSSSSSSSSSSSS 657
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 OY 760 GTCCACTACGCGTGAACGCTGTGGTCCGCGCGCGGCGGCGGCGGCGGCGGCGGCGG 819
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 DB 656 SMSASSSSSSSSSSSSSSSSSSSSSSSAGCBMSWSSGSGSGSVASSGMSVSSGGRSS 597
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 OY 820 GG 821
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 DB 596 GS 595
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 6
 LOCUS AM827060 616 bp mRNA EST 17-MAY-2000
 DEFINITION IK57H09.y1 Zebrafish adult retina cDNA Danio rerio 5' similar
 to gb:X04526.cds2 GUININE NUCLEOTIDE-BINDING PROTEIN G(11)/G(S)/G(T)
 BETA SUBUNIT (HUMAN);, mRNA sequence.
 ACCESSION AM827060

VERSION	AM827060.1	GI:7920137
KEYWORDS	EST.	
SOURCE	zebrafish.	
ORGANISM	Danio rerio.	
REFERENCE	Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi; Cypriniformes; Cyprinidae; Rasbora; Danio.	
AUTHORS	Clark, M., Johnson, S.L., Lehnach, H., Lee, R., Li, F., Marra, M., Eddy, S., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shih, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.	
TITLE	Mashu zebrafish EST Project 1998	
JOURNAL	Unpublished (1998)	
COMMENT	Contact: Stephen L. Johnson Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA Tel: 314 286 1800 Fax: 314 286 1810 Email: zbrfish@wustl.edu Library constructed by: Susan E. Brockerhoff DNA Sequencing by: Washington University Genome Sequencing Center Clone Distribution Resource: zenitum@primatetenbank, Berlin, Germany (web address: www.rzpd.de) Seq primer: T3 ET from Amersham High quality sequence stop: 427. Location/Qualifiers	
FEATURES	1. 616 /organism="Danio rerio" /strain="wild-type" /db_xref="taxon:7955" /clone_lib="Zebrafish adult retina cDNA" /sex="mixed" /dev_stage="1-2 years" /lab_host="E.Coli XL1-Blue MRF" (XL1-Blue MRF)" /note="Vector: Lambda ZAP II (pBluescript SK-); Site-1: EcoRI; Site-2: SalI; This Zebrafish library was constructed by Dr. Susan E. Brockerhoff (email: sbrocker@erdc.washington.edu) RZPD library number: 760"	
BASE COUNT	126 a 184 c 174 g 132 t	
ORIGIN		
Query Match	2.5%;	Score 43.6; DB 121; Length 616;
Best Local Similarity	48.1%;	Pred. No. 0.91;
Matches 124; Conservative	0;	Mismatches 134; Indels 0; Gaps 0
QY	366 CACCGTGAACAGCTTTGGGAGCGGACCCGGCGATGGCGCTGTACGGGACCAACGTTTAA	425
Db	78 CCCCTGCGCTCCCTCGTGGGTGATGACCTGTGCGTACGCGCGCGCTCCGGGAATCACTGTCG	137
QY	426 CTTTGTTCGGGGAGAACACCACTGCTGCCCTCCGACACCGCAACTGGCCCAAGTACGCTT	485
Db	138 GTGGGGAGGTTTGGACACATCTGCTCCATCTTACCACTGTAAGACCCGCGAGGGGAACGT	197
QY	486 CGAGCTGACCGCGGCGCAAGGCGAAGACATGTGTTTGAATCTGTGGGCGCGATCGTGGC	545
Db	198 GCGGCTGACGCGGAGAGCTAGCGGACACACAGATTATCTGTCCTCTGCTTTCCTGGA	257
QY	546 AAACGGCGTGAATCGTGGCGGTTTGCACCTGCCAATAATCTGCGGCTCTTTGTCTC	605
Db	258 TGATTAACCAATGTGTGACCAAGCTCAGCGACACCAACCACTGTGCTGTGTGGACATCGAGAC	317
QY	606 GGGCGACAGATCGGCGAC	623
Db	318 AGGCGACAGACGACGACAC	335
RESULT	7	
LOCUS	BC308084	662 bp mRNA EST 22-FEB-2001

DEFINITION	fm56f02.y1 zebrafish adult retina cDNA Danio rerio CDNA clone 14956f02.y1 similar to SW:G8B1 HUMAN P04901 GUANINE NUCLEOTIDE-BINDING PROTEIN G(I)/G(S)/G(T) BETA SUBUNIT 1 ; mRNA sequence.					
ACCESSION	BG308084.1 GI:13105611					
VERSION	EST.					
KEYWORDS	zebrafish.					
SOURCE	Danio rerio					
ORGANISM	Eukaryotes; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi; Cypriniformes; Cyprinidae; Rasbora; Danio.					
REFERENCE	Clark,M., Johnson,S.L., Lehrach,H., Lee,R., Li,F., Marra,M., Eddy S., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood, K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Page,D., Harvey,N., Shuk,R., Ritter,E., Kohn,S., Shin,T., Jackson,T., Cardenas,M., McCann,R., Waterston,R. and Wilson.R.					
TITLE	Washu Zebrafish EST Project 1998					
JOURNAL	Unpublished (1998)					
COMMENT	Contact: Stephen L. Johnson Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA Tel.: 314 286 1800 Fax: 314 286 1810 Email: zbrafish@wustl.wustl.edu Library constructed by: Susan E. Brockerhoff DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: ResourceCenterumPrimaratenbank, Berlin, Germany (web address: www.rzpd.de) Seq primer: T3 ET from Amersham High quality sequence stop: 412. Location/Qualifiers 1. 662 /organism="Danio rerio" /strain="wild-type" /db_xref="taxon:7955" /clone="14956f02.y1" /clone_1ib="Zebrafish adult retina cDNA" /sex="mixed" /dev_stage="1-2 years" /lab_host="F. coli XL1-blue MRF' (XL1-blue MRF')" /note="vector: Lambda Zap II (pluscript SK-)"; Site_1: ECORI; Site_2: SalI; This Zebrafish library was constructed by Dr. Susan E. Brockerhoff (email: sbrocke@u.washington.edu) RZPD library number: 760"					
BASE COUNT	161 a 175 c 194 g 132 t					
ORIGIN						
Query Match	2.5%; Score 43.6; DB 175; Length 662;					
Best Local Similarity	48.1%; Pred. No. 0.92;					
Matches 124; Conservative	0; Mismatches 134; Indels 0; Gaps 0;					
OY	366	CAGCGTGAACAGTTTGCGGAGCCAGCCGCCATGGCGGTGACGCACCAACCTTA	425			
Db	353	CCGCGTCGCTCCTCGTGGGTATACCTGTCGACCGCGCGTCCGGAACTACGTGGC	412			
OY	426	CTTTGTTTCGTGGGACMACACACTGATGACCCTGCACACCGCATGCGCAATGACGT	485			
Db	413	GTTGGGAGGTTTGAGACAACATGTGTCATACAAACCTGAAAGACCGGAGGGAACGT	472			
OY	486	CGAGCTGACCGCGGCAAGCGAAGACATGTTTCGACTGTCGGGCGCATCGTGGC	545			
Db	473	GCGGCTGACCGCGAGACTAGCCGGACACAGAGTTATTCTGTCTGCTGTTCTCTGA	532			
OY	546	AAACGGCGTAGATGTTGCCGCTGACCTGCACCAATACCGCGTGGCGTCTTGTTC	605			
Db	533	TGATTAACCATATGTGTACCACTCACGCGAACACCACTGTGCTGTGGACATCGAGAC	592			
OY	606	GAGCCACGACGCGGCCAC	623			

Db	593	AGGCCAGCAGACACCAC	610
RESULT#	8		
LOCUS	BEG02586		
DEFINITION	BEG02586 HVSMEH0100C21f Hordeum vulgare 5-45 DAP spike EST library HVCDNA0009 (5 to 45 DAP) Hordeum vulgare cDNA clone HVSMEH0100C21f, mRNA sequence.	mRNA	EST 02-MAR-2001
ACCESSION	BEG02586		
VERSION	BEG02586.2		
KEYWORDS	GI:13190506		
SOURCE	barley. Hordeum vulgare		
ORGANISM	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae; Hordeum. 1 (bases 1 to 740) Wing,R., Close,T.J., Kleinhefs,A., Wise,R., Begum,D., Frisch,D., Yu ,Y., Anderson,H., Dale,J., Henry,D., Kernodle,S., Palmer,M., Rambo ,T., Saski,C., Schwartzbeck,J., Simmons,J., Choi,D.W., Main,D. and Wood,T. Development of a genetically and physically anchored EST resource for barley genomics Unpublished (2000) On Aug 21, 2000 this sequence version replaced gi:9860147. Contact: Wing RA Clemson University Genomics Institute Clemson University 100 Jordan Hall, Clemson, SC 29634, USA Tel.: 864 656 7288 Fax: 864 656 4293 Email: rwing@clemson.edu Seq primer: AATTAACCTCATCAAAAGG High quality sequence stop: 532. Location/Qualifiers		
FEATURES			
source	1..740		
	/organism="Hordeum vulgare"		
	/cultivar="Morex"		
	/db_xref="taxon:4513"		
	/clone="HVSMEH0100C21f"		
	/clone_1ib="Hordeum vulgare 5-45 DAP spike EST library HVCDNA0009 (5 to 45 DAP)"		
	/tissue_type="5-45 DAP Spike"		
	/lab_host="SOIR"		
	/note="Vector: lambdaZAP; Site_1: EcoRI; Site_2: XhoI"		
BASE COUNT	134 a 259 c 226 g 121 t		
ORIGIN			
Query Match	2.5%; Score 43.6; DB 137; Length 740;		
Best Local Similarity	46.2%; Pred. No. 0.94,		
Matches 145; Conservative	0; Mismatches 169; Indels 0; Gaps 0.		
Oy	240 CCAAGTCACGGCCCGATGCATGACAGCGGCGTCAATGTGGAACAACCCGGGAGCGTGAT	299	
Db	118 CAAGAAGAGGGCGCACCGCAGCGCCGCGCAGACAAGTGCCGCTTGTTGGACACTT	177	
Oy	300 CCAGGCGCATGACAGCCAAAAGTAGTGATCTGTGGGAACACCGCCGCAACTGCGCAA	359	
Db	178 CTACACACTCTACACGACATCATAGTAGGGGCTGGGGCCAGTCCCTTCACCTTCGCGC	237	
Oy	360 CATGCGCAGCGTGAACAGATTGGGAGGCGGACCGCGCATGCGCGCTGTACGGACCAA	419	
Db	238 CTCCTCCCCCGCGCTCCCACCGCAGCGCACCGCGCTGCACAGAGAACGGCTGCGCA	297	
Oy	420 CGTTTACTTTGTTGCTGGAGACAACCACTGTGCGCTTGACACCGCAACTGGCCAAGT	479	
Db	298 CCTGCTGCGCAGACAGCGCCGGGCGCAGCGCTGCAGCGTGCAGTGGCGGTGACGCTGC	357	
Oy	480 GAGTTTGAGGTGACCGGGGGCCAAAGCAAGCATGGTTTGCAACTGTCGGGCGCGAT	539	
Db	358 CATTGGCGGCAATGCGCGCCACTAGCGGCCCACTTGTTGGCATTCACATCAACAGATA	417	

[illegible]

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Db      151  MMCMCMSTCCMCGCCGYCC 134

RESULT  10
BE211954
LOCUS   894024H07.v1 C. reinhardtii CC-1690, normalized, lambda zap II
DEFINITION Chlamydomonas reinhardtii cDNA, mRNA sequence.
ACCESSION BE211954
VERSION   BE211954.1 GI:8828112
SOURCE    EST.
ORGANISM  Chlamydomonas reinhardtii.
           Chlamydomonas reinhardtii.
           Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
           Chlamydomonadales; Chlamydomonadales; Chlamydomonadales;
           1 (bases 1 to 308)
REFERENCE Grossman,A., Davies,J., Federspiel,N., Harris,E., Lefebvre,P.,
AUTHORS  McDermott,J.P., Silflow,C., Stern,D. and Surzycki,R.
TITLE     Analyses of the Chlamydomonas reinhardtii Genome: A Model,
           Unicellular System for Analyzing Gene Function and Regulation in
           Vascular Plants: project phase 2
JOURNAL   Unpublished (2000)
COMMENT   Contact: Elizabeth H. Harris
           DCMB Box 91000
           Duke University
           Durham, NC 27708-1000, USA
           Tel: 919 613 8164
           Fax: 919 613 8177
           Email: chlamy@duke.edu.
FEATURES
SOURCE    Location/Qualifiers
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             /db_xref="taxon:3055"
             /clone_lib="C. reinhardtii CC-1690, normalized, lambda zap
             II"
             /note="vector: pluescript II SK-; Site_1: EcoRI; Site_2:
             XhoI; This library, constructed by John Davies and Jeffrey
             McDermott, combines cDNAs from CC-1690 cells grown to
             mid-log phase in YAP (acetate-containing) medium in the
             light, YAP medium in the dark, HS (minimal) medium in
             ambient levels of CO2 and HS medium bubbled with 5% CO2.
             PolyA mRNA was purified from each sample, pooled and cDNA
             synthesized. The cDNA was directionally cloned into lambda
             zap II (Stratagene) in the EcoRI (5') and XhoI (3') sites.
             pluescript II SK- plasmids were excised from the lambda
             zap clones by superinfection with Exassist (Stratagene)
             phage. The library was normalized using method 4 described
             in Bonaldo et al (1996) Genome Research 6: 791-806."
BASE COUNT  54 a      110 c      101 g      43 t
ORIGIN

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[illegible]

Query Match	2.5%	Score 43	DB 146	Length 759
Best Local Similarity	42.5%	Pred. No. 1.3		
Matches 223	Conservative	0	Mismatches 302	Indels 0
			Gaps	0
QY	CGCGCGTCGGAAACCCACGCGGACCCCGGGCGGACCGTGTACGACGACAGACCCGTT	847		
Db	53 CGGGGACGAGGGGCCGTTCTCTCAACATGTCTGTCTCAACATCTATGGGGCCCAAGAACCA	112		
QY	848 TCGCGGTGCTCTCTTGACAGCGGCGAGATTGTCTGTGGCGTACACCAACCCCTGCCGGGACA	907		
Db	113 TGGAGATCGGCGCTTACACAGGSGCTACTCCGTGTCTGGCACCGGCGTGGCCATCCCGAGG	172		
QY	908 ACTGGGACCGAGATGCATGTTGAGATGATGTGTACCAATGTGGATGTCCAAACCTTCA	967		
Db	173 ACGGACCACTCTTTGGGCATGAGACATCAACCGCGAAGACTAGAGACTGGGGCTCCCTGTGA	232		
QY	968 CCGAGATGGAGATGTGCTGATGCATCAACCGGAGCGCGCAACTGGGGAGCTGTCCGGTGG	1027		
Db	233 TCGAGAAAGGCGCGGTGGGCGCACAAAGATGCATCTCCGGAGAGCGCCGGCGCTCCCGCTCC	292		
QY	1028 TGACCGGCGTTCCGTGTCAAAACCGGACCAATGTGGCACTGTGACGCCGGAACCGGGGAAT	1087		

